

Gencore version 4.5
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OM protein - protein search, using sw model
Run on: September 28, 2000, 17:01:17 ; Search time 47.45 Seconds
(without alignments)
220.092 Million cell updates/sec

Title: US-09-142-613-1

Perfect score:

Sequence: 1 MAEPROFEVEMEDHAGQDMY.....SPQLATLADEVSASLAKOGL 441

Scoring table: BLOSUM62 Gapop 10.0 , Gapext 0.5

Searched: 188963 seqs, 23686105 residues

Total number of hits satisfying chosen parameters: 188963

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A_Geneseq_36:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	2295	100.0	441	1	W34856 Human tau protein.
2	2262	98.6	441	1	W58810 Human tau protein.
3	2223	96.9	441	1	W05282 Human tau protein.
4	1983	86.4	390	1	W05283 Truncated human tau protein.
5	1719.5	74.9	352	1	P91294 Paired helical fil.
6	1719.5	74.9	352	1	R91294 Human tau-protein.
7	739	32.2	1717	1	W23331 Neuroblastoma indi.
8	733	31.9	140	1	W05285 Human tau protein.
9	713.5	31.1	1831	1	W23329 Microtubule-assoc1
10	593	25.8	112	1	R76937 Microtubule-assoc1
11	563	24.5	106	1	R92516 Fragment of microt
12	551	24.0	140	1	W05286 Human tau protein
13	501	21.8	95	1	W05284 Sequence of human
14	364	15.9	67	1	R59837 Human tau protein
15	364	11.8	55	1	W34876 Tau40 epitope (es
16	270	9.5	42	1	R98431 Peptide phosphoryl
17	185	8.1	34	1	R61330 Human tau protein
18	185	8.1	34	1	W34875 Malaria1 PfEMP3 ep
19	172.5	7.5	455	1	R46605 Plasmodium falcipa
20	172.5	7.5	1663	1	W46608 MSF Precursor. New
21	159.5	6.9	1404	1	R26049 Group B Streptococ
22	157	6.8	984	1	R85782 Mutant C-beta prot
23	157	6.8	1093	1	W40540 Mutant C-beta prot
24	157	6.8	1099	1	W40539 Mutant C-beta prot
25	157	6.8	128	1	W40539 Group B Streptococ
26	157	6.8	164	1	R85781 Group B streptococ
27	157	6.8	164	1	R85781 Mutant C-beta prot
28	157	6.8	164	1	W40541 C. thermocellum OI
29	154	6.7	1664	1	W43106 Human SIAP-130. Nu
30	153	6.7	783	1	W770586 Mouse neuron restr
31	150.5	6.6	976	1	W02289 Human secreted pro
32	150	6.5	649	1	W5783 R66450 AF-4 protein (enco
33	150	6.5	649	1	R66451 AF-4 protein (enco

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9	713.5	31.1	1831	1	W23329 Microtubule-assoc1
10	593	25.8	112	1	R76937 Microtubule-assoc1
11	563				

Db	361	THPPGGGNKKIEHKLTIRENAAKTDHGAEVYKSPVVGDSIPRHLNSVSTGSIDAY	420	
Qy	421	DSPOLATLADEVASASLAKOGL	441	W0282
Db	421	DSPOLATLADEVASASLAKOGL	441	W05282
RESULT	2			standard; Protein; 441 AA.
R58810				AC R58810;
ID				DT 27-MAR-1995 (first entry)
				DE Human tau protein.
				KW Tau; cerebrospinal fluid; immunoassay; antibody; detection;
				KW diagnosis; central nervous system; CNS; cytopathies; cytopathy;
				KW Alzheimer's disease.
				OS Homo sapiens.
PN				PN WO911850-A.
PD				PD 18-AUG-1994.
PF				PF 10-FEB-1994; JP-004133.
PA				PA (TEIJIN LTD.
PI				PI Eguchi R, Rosoda K, Kobayashi S, Kubota T, Mori H;
PT				PT Nakamoto T;
DR				DR WPI: 94-279910/34.
PT				PT Sandwich immunoassay of tau protein in cerebrospinal fluid - for
PS				PS diagnosis of Alzheimer's disease and other CNS cytopathies
				Claim 1; Page 16-18; 36PP; Japanese.
				Detection of the human tau protein (or fragments of it) in samples
CC				CC of cerebrospinal fluid enables the diagnosis of central nervous
CC				CC system cytopathies such as Alzheimer's disease. Detection is
CC				CC performed using labelled antibodies which recognise sites within the
CC				CC region defined by the amino acid residues 251-441. The antibodies
CC				CC are preferably polyclonal.
SQ				Sequence 441 AA;
Query Match	98.6%	Score 2262; DB 1; Length 441;		
Best Local Similarity	99.1%	Pred. No. 2.7e-150;		
Matches	439;	Conservative	0;	Mismatches 0;
				Indels 4; Gaps 2;
Qy	1	MAEPROEFEVMEHDAGQDGYTGLGRDKDQGYTMH--QEGDDAISLKESPLOQTPEPDSE	58	PSI: 96-4557045.
Db	1	MAEPROEFEVMEHDAG--TYGLGDRKDQGYTMHDOEQDTAGLKESPLQPTEDGSE	58	DR N-FSDB; T3951.
Qy	59	PGSETSDAKSTPPTEDVTLPLVGDGPKQAQPHTEPEGTTAEEAGIGDPSLEDA	118	PT Assay for inhibitors of tau-tau interaction - used for identifying
Db	59	PGSETSDAKSTPPTEDVTLPLVGDGPKQAQPHTEPEGTTAEEAGIGDTPSLEDA	118	PT capping agents, partic. phenothiazine capping, for treating pathological
Qy	119	AGHTQARAVSKSKDGTGSDDKAKAGDKTKTATPRGAAPPQKQANATRIPAKTPPA	178	PT tau-tau or neurofilament aggregation.
Db	119	AGHTQARAVSKSKDGTGSDDKAKAGDKTKTATPRGAAPPQKQANATRIPAKTPPA	178	Example 2; Page 53-54; 97PP; English.
Qy	179	PKTPSSCEPPPKSDRSQGSSPGPQGSRSPRLPPTPRTSPKKAVVRTPPKSPSS	238	CC Defecting an agent which modulates or inhibits tau-tau protein
Db	179	PKTPSSCEPPPKSDRSQGSSPGPQGSRSPRLPPTPRTSPKKAVVRTPPKSPSS	238	CC association comprises contacting two tau proteins, distinct from
Qy	239	AKSRLQTAAPVMPDLKNVSKKGSTEKLHQGGGKVQINKLDSLNVQSKGSDNK	298	CC each other yet capable of binding to the other and where one of the
Db	239	AKSRLQTAAPVMPDLKNVSKKGSTEKLHQGGGKVQINKLDSLNVQSKGSDNK	298	CC tau proteins is labelled, in the presence of the agent suspected of
Qy				CC being capable of modulating or inhibiting tau-tau interaction.
Db				CC Agents identified as being modulators or inhibitors of tau-tau
Qy				CC interaction may be used for the prophylaxis and treatment of
Db				CC Alzheimer's disease, motor neurone disease, Lewy body disease,
Qy				CC Pick's disease or progressive supranuclear palsy.
SQ				Sequence 441 AA;
Query Match	96.9%	Score 2223; DB 1; Length 441;		
Best Local Similarity	98.0%	Pred. No. 1.4e-147;		
Matches	434;	Conservative	0;	Mismatches 5;
				Indels 4; Gaps 2;
Qy	1	MAEPROEFEVMEHDAGQDGYTGLGRDKDQGYTMH--QEGDDAISLKESPLOQTPEPDSE	58	PSI: 96-4557045.
Db	1	MAEPROEFEVMEHDAG--TYGLGDRKDQGYTMHDOEQDTAGLKESPLQPTEDGSE	58	DR N-FSDB; T3951.
Qy	59	PGSETSDAKSTPPTEDVTLPLVGDGPKQAQPHTEPEGTTAEEAGIGDPSLEDA	118	PT Assay for inhibitors of tau-tau interaction - used for identifying
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Qy	179	PKTPSSCEPPPKSDRSQGSSPGPQGSRSPRLPPTPRTSPKKAVVRTPPKSPSS	238	CC Defecting an agent which modulates or inhibits tau-tau protein
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Qy	239	AKSRLQTAAPVMPDLKNVSKKGSTEKLHQGGGKVQINKLDSLNVQSKGSDNK	298	CC each other yet capable of binding to the other and where one of the
Db	239	AKSRLQTAAPVMPDLKNVSKKGSTEKLHQGGGKVQINKLDSLNVQSKGSDNK	298	CC tau proteins is labelled, in the presence of the agent suspected of
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Db				CC Alzheimer's disease, motor neurone disease, Lewy body disease,
Qy				CC Pick's disease or progressive supranuclear palsy.
SQ				Sequence 441 AA;
Query Match	98.6%	Score 2262; DB 1; Length 441;		
Best Local Similarity	99.1%	Pred. No. 2.7e-150;		
Matches	439;	Conservative	0;	Mismatches 0;
				Indels 4; Gaps 2;
Qy	1	MAEPROEFEVMEHDAGQDGYTGLGRDKDQGYTMH--QEGDDAISLKESPLOQTPEPDSE	58	PSI: 96-4557045.
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Db				CC Agents identified as being modulators or inhibitors of tau-tau
Qy				CC interaction may be used for the prophylaxis and treatment of
Db				CC Alzheimer's disease, motor neurone disease, Lewy body disease,
Qy				CC Pick's disease or progressive supranuclear palsy.
SQ				Sequence 441 AA;

RESULT	4	DT	18-DRC-1989 (first entry)
W05283		DE	Paired helical filament (PHF) core protein.
ID	W05283; standard; Protein: 390 AA.	KW	Alzheimer's disease;
AC		KW	Paired helical filament (PHF) core protein: Alzheimer's disease;
DT	20-DEC-1996 (first entry)	OS	neurofibrillary tangles.
DE	Truncated human tau protein.	OS	Homo sapiens
KW	Tau protein; inhibition; modulation; prophylaxis; treatment;	PN	W080395-A.
KW	Alzheimer's disease; motor neurone disease; Lewy body disease;	PD	05-MAY-1989.
KW	progressive supranuclear palsy; Pick's disease.	PF	19-OCT-1988; G00867.
OS	Homo sapiens.	PR	19-OCT-1987; GB-024412.
PN	W09610766-A1.	PA	(MEDI) Medical Research Council.
PD	03-OCT-1996.	PI	Wischik CM, Milstein C, Klug A;
PF	25-MAR-1996; E01307.	DR	WPI: 89-150854-20.
PR	27-MAR-1995; GB-006197.	PT	Paired helical filament core protein - used for providing reagents
PA	(HOFF) HOFFMANN LA ROCHE & CO AG F.	PT	sensitive to neurofibrillary tangles used for diagnosing Alzheimer's
PI	Edwards PC, Harrington CR, Klug A, Roth M, Wischik CM;	PT	disease.
DR	WPI: 96-4557045.	PS	Disclosure: fig 1; 29PP: English.
PT	Assay for inhibitors of tau-tau interaction - used for identifying	CC	Paired helical filament core protein was sequenced from DNA obtained
PT	CDDPs, paricic, phenothiazine cddps, for treating pathological	CC	from brain tissue contg. Alzheimer neurofibrillary tangles. The protein
PT	tau-tau or neurofilament aggregation	CC	can be used to make MAb's to the PHF core or nucleotide probes, used to
PS	Claim 11; 9/PP: English.	CC	diagnose Alzheimer's disease. The protein sequence QIVKIP (AAs 218-223)
CC	Detecting an agent which modulates or inhibits tau-tau protein	CC	was used to design the probes.
CC	association comprises contacting two tau proteins distinct from	CC	See also N9107.
CC	each other yet capable of binding to the other and where one of the	SQ	Sequence 352 AA;
CC	tau proteins is labelled, in the presence of the agent suspected of		
CC	being capable of modulating or inhibiting tau-tau interaction.		
CC	Agents identified as being modulators or inhibitors of tau-tau		
CC	interaction may be used for the prophylaxis and treatment of		
CC	Alzheimer's disease, motor neurone disease, Lewy body disease,		
CC	Pick's disease or progressive supranuclear palsy. This sequence of		
CC	the human tau protein is truncated at amino acid residue 390. The		
SQ	full length protein is given in W05282.		
Query Match	86.4%; Score 1983; DB 1; Length 390;	Query Match	74.9%; Score 1719.5; DB 1; Length 352;
Best Local Similarity	98.0%; Pred. No. 6.3e-131;	Best Local Similarity	78.6%; Pred. No. 1.3e-112;
Matches	384; Conservative 0; Mismatches 4; Indels 4; Gaps 2;	Matches	348; Conservative 0; Mismatches 12; Indels 93; Gaps 4;
QY	1 MAEPROFEVMEHDAGQDTYGLGDRKDQGGYTMH-~OEGDTDAGLKESPLOPTEPDGSEE 58	QY	1 MAEPROFEVMEHDAGQDTYGLGDRKDQGGYTMH-~OEGDTDAGLKESPLOPTEPDGSEE 58
Db	1 MAEPROFEVMEHDAG-~TYGLGDRKDQGGYTMH-~OEGDTDAGLKESPLOPTEPDGSEE 58	Db	1 MAEPROFEVMEHDAG-~TYGLGDRKDQGGYTMH-~OEGDTDAGLKESPLOPTEPDGSEE 58
QY	59 PGSESDAKSTPTAEDVTAPLVDEGAPKGQAAQPHTEPEGTAAEIGGIDTPSLEDA 118	QY	59 PGSESDAKSTPTAEDVTAPLVDEGAPKGQAAQPHTEPEGTAAEIGGIDTPSLEDA 118
Db	45 -----REEGIDTPSLEDA 50	Db	45 -----REEGIDTPSLEDA 50
QY	119 AGHYTOARAVSKSKDGTGSDDKAKAGDKTKATPRGAAPRQKGQANTRIPTPPA 178	QY	119 AGHYTOARAVSKSKDGTGSDDKAKAGDKTKATPRGAAPRQKGQANTRIPTPPA 178
Db	61 AGHYTOARAVSKSKDGTGSDDKAKAGDKTKATPRGAAPRQKGQANTRIPTPPA 120	Db	61 AGHYTOARAVSKSKDGTGSDDKAKAGDKTKATPRGAAPRQKGQANTRIPTPPA 120
QY	179 PTKTPSSGEPPKSKDRSGYSSPSPGTPGSRSTPSLTPPTEPKKAWVRTPPKSPSS 238	QY	179 PTKTPSSGEPPKSKDRSGYSSPSPGTPGSRSTPSLTPPTEPKKAWVRTPPKSPSS 238
Db	121 PTKTPSSGEPPKSKDRSGYSSPSPGTPGSRSTPSLTPPTEPKKAWVRTPPKSPSS 180	Db	121 PTKTPSSGEPPKSKDRSGYSSPSPGTPGSRSTPSLTPPTEPKKAWVRTPPKSPSS 180
QY	239 AKSRLQTAQVPMPPDLKNVSKISTENTKHQPGGKVQLINKLDSNVQSKGSKDNK 298	QY	239 AKSRLQTAQVPMPPDLKNVSKISTENTKHQPGGKVQLINKLDSNVQSKGSKDNK 298
Db	181 AKSRLQTAQVPMPPDLKNVSKISTENTKHQPGGK----- 216	Db	181 AKSRLQTAQVPMPPDLKNVSKISTENTKHQPGGK----- 216
QY	299 HVPGGGSTVQIVYKVVDLKVTS CGS LNIHH PGG GQEV KSEK LDF KDR VQSKIGSLD 358	QY	299 HVPGGGSTVQIVYKVVDLKVTS CGS LNIHH PGG GQEV KSEK LDF KDR VQSKIGSLD 358
Db	217 -----VOIVYKVVDLKVTS CGS LNIHH PGG GQEV KSEK LDF KDR VQSKIGSLD 269	Db	217 -----VOIVYKVVDLKVTS CGS LNIHH PGG GQEV KSEK LDF KDR VQSKIGSLD 269
QY	359 NITHPGGGNKKIEHKUTPRENAKADHGAIWVYKPVWSDDTSRHLNSWNSSTGSD 418	QY	359 NITHPGGGNKKIEHKUTPRENAKADHGAIWVYKPVWSDDTSRHLNSWNSSTGSD 418
Db	270 NITHPGGGNKKIEHKUTPRENAKADHGAIWVYKPVWSDDTSRHLNSWNSSTGSD 329	Db	270 NITHPGGGNKKIEHKUTPRENAKADHGAIWVYKPVWSDDTSRHLNSWNSSTGSD 329
QY	419 MVDSPOLATLADEVASASTAKQI 441	QY	419 MVDSPOLATLADEVASASTAKQI 441
Db	330 MVDSPOLATLADEVASASTAKQI 352	Db	330 MVDSPOLATLADEVASASTAKQI 352
RESULT	5	RESULT	6
R32708		R32708	
ID	R32708; standard; Protein: 352 AA.	ID	R32708; standard; Protein: 352 AA.
AC		AC	15-JUN-1993 (first entry)
DT		DE	Human tau-protein.
DE		KW	Alzheimer's disease; diagnosis; subtyping; monitoring; assay.
KW		OS	Homo sapiens.
OS		PN	W0930365-A.
PN		PD	18-FEB-1993.
PD		PF	03-AUG-1992; U06382.
RESULT	5		
P91294			
ID	P91294; standard; protein: 352 AA.		
AC			
P91294			
10-MAR-1993 (revised)			

PR 01-AUG-1991; US-738778.
 PA (VOOR/) VOORHEIS P H.
 PI Voorheis PH;
 WPI; 93-076670/09.
 DR N-PSDB; Q37305.

PT Method for diagnosing, subtyping and monitoring Alzheimer's disease - by assaying a sample of body fluid for the presence of a tau-peptide using an anti-tau antibody
 Disclosure; Fig 1; 43pp; English.
 The sequence is that one form of human tau protein (from Goedert et al., PNAS USA 85: 4051-4055) which was used for the prodn. of anti-tau peptide antibodies. These are used as part of a method for diagnosing, subtyping or monitoring Alzheimer's disease by assaying a sample of body fluid for the presence of a tau-peptide using an anti-tau antibody or the presence of an anti-tau-peptide diagnosis of Alzheimer's disease and in following the course of the disease and treatment.

CC Sequence 352 AA;

Query Match 74.9%; Score 1719.5; DB 1; length 352;
 Best Local Similarity 78.6%; Pred. No. 1.3e-11; Mismatches 348; Conservative 0; Indels 93; Gaps 4; Matches 348; Mismatches 0; Indels 93; Gaps 4;

QY 1 MAEPRQFEEVMEHDAGQDTYGLGDRKDGGYTMH-QEGDTDGLKESPLQPPTEDGSEE 58
 Db 1 MAPRQREVMEDHAG-TYGLGDRKDGGYTMH-QEGDTDGLK----- 44

QY 59 PGSEETSDAKSTPAAEDVTPALVDEGAPQRQAAQPHTEIPEGTAEEAGIGDPSLEDA 118
 Db 45 -----AEGAGIPTPSLEDA 60

QY 119 AGHVTQARMSKSKDGGSDKKAKGADGKTKATPRGAAPRQKGANATRIPAKKPPA 178
 Db 61 AGHVTQARMSKSKDGGSDKKAKGADGKTKATPRGAAPRQKGANATRIPAKKPPA 120

QY 179 KPPSSCEPKPGDRSGYSSPSPCGSRSTPSLTPTRPEPKVAVWTPPKSPSS 238
 Db 121 PKPPSSCEPKPGDRSGYSSPSPCGSRSTPSLTPTRPEPKVAVWTPPKSPSS 180

QY 239 AKSRLQATAPVPMEDLKNVSKIGSTENIKHQPGGKVQLINNLDLSNVQSKCGSKONIK 298
 Db 181 AKSRLQATAPVPMEDLKNVSKIGSTENIKHQPGGK----- 216

QY 299 HVPGGGSVQIVVYLPVDLKVTSKCGSLGNINHHPPGGGOEVKESEKLDKDRYOSKICSLD 358
 Db 217 -----VQIVVYLPVDLKVTSKCGSLGNINHHPPGGGOEVKESEKLDKDRYOSKICSLD 269

QY 359 NITRHVGCGNKKIETHKLTFREAKAKTDHGAIIVYKSPVWSDTSRHLNSNSTSID 418
 Db 270 NITRHVGCGNKKIETHKLTFREAKAKTDHGAEIVYKSPVWSDTSRHLNSNSTSID 329

QY 419 MVDSPQLATLADDEVASLAKQGL 441
 Db 330 MVDSPQLATLADDEVASLAKQGL 352

RESULT 7
 ID W23331 standard; Protein; 1717 AA.
 AC W23331; (first entry)
 DT 23-MAR-1998
 DE Neuroblastoma indicative isoform of MAP2 (NB-MAP2).
 KW microtubule-associated Protein 2; MAP2; neuroblastoma; human; Homo sapiens.
 FH Location/Qualifiers
 Key
 Misc_difference 1711
 /Note- "encoded by TGA"
 Misc_difference 1716
 FT WO9727323-A1. /Note- "encoded by TAG"
 PN

Query Match 32.2%; Score 739; DB 1; length 1717;
 Best Local Similarity 38.7%; Pred. No. 2e-43; Mismatches 182; Conservative 57; Indels 126; Gaps 13; Matches 182; Mismatches 57; Indels 126; Gaps 13;

QY 48 LQPTEDCSEERGS-----ETSDAKSTPAAEDVTPALVDEGAPQRQAAQPHTEIPE 99
 Db 1291 VOTTDDEG---BGSGHSYRFAALEQEPVERPSPHDEEEFEVEAA--EAQAEPRDGSP 1345

QY 100 GTAAEENAGIGDPSLEDAEAGHVTQARMSKSKDGGSDKK----- 140

Db 1346 AFASPE-----REEVIASEKPYTIDYKDETTIDSIMADSILWDTQAGGSEA 1395

QY 141 -----KARGADGKTKATPRGAP-----FGOKG----- 169

Db 1397 LAPSVFQKAQDKVSDGVTKPSKPEKRSSLPRSSILPPLRRGSGDRDENSESLSNSSLSSAR 1456

QY 170 RAPAKT-----PARKPSS---GPBKSDRSYKSSPSPGTGSRSTPSR 216
 Db 1457 RTRSEPIRARRACKSGSTPTPFGSTATPTGTPPSYSSR---TPTGTPGTP-SYPTPTPHT 1511

QY 217 TPP-----TREPKVAVWTPPKSPSSAKSRLQATAPVPMEDLKNVSKIGSTENIKHQPG 271
 Db 1512 GPKSALIWPSEPKKVAIRTPPKSPSLTPKQLRLLNPDLKNTSKIGSTDNIKYQK 1571

QY 272 GSKVQINKLNUYNSVQSKCGSKDNTRHVPGGGSVQIVVYLPVDLKVTSKCGSLGNINHH 331
 Db 1572 GGVOVTKKIDLSH----- 1600

QY 332 PSQGQVKSEKLFKQYQSKIGSLDNITHPGCGNKKIETHKLTFREAKAKTDHGAE 391

Db	1601 PGGRKVKLESVQLDFKEKAQVKGSLDNAHYPGGNTKIDSQKLNFREHAKRDHGAE	1660	PF	23-JAN-1997; E00320.
OY	392 IVVKSPVYSGDTSPLRHSNVSTGSDIDAVDSPLATLDEVSASLAQGL 441		PR	23-JAN-1996; E0100930.
ID	W05285; standard; Protein; 140 AA.		PA	(PLAC) MAX PLANCK GES FOERDERUNG WISSENSCHAFTEN.
AC	W05285;		Kirsch, J.; Kurek, R;	
DR	1661 IITOSPGISSVASPRRLSNVSSGGINLESPOLATLAEDVTRALAKGL 1710		WPI; 97-39707/36.	
RESULT	8		DR	N-PADB: T64950.
W0285			PT	Diagnostic agents for detecting neuroblastoma specific isoform of microtubule-associated protein - for diagnosis or monitoring of neuroblastoma, are primers, probes or antibodies, also new
DT	20-DEC-1996 (first entry)		PT	therapeutic antisense sequence.
DE	Human tau protein core sequence.		PS	Disclosure; Fig 2; 34pp; English.
KW	Tau protein; inhibition; modulation; prophylaxis; treatment; Alzheimer's disease; motor neurone disease; Lewy body disease;		CC	This is the human microtubule-associated protein 2 (MAP2). A 250 KD isoform of this 270 kb MAP2 is indicative of neuroblastoma. This isoform NB-MAP2 arises from alternative splicing of the primary MAP2 transcripts.
KW	progressive supranuclear palsy; Pick's disease; ss.		CC	Diagnostic agents for detecting NB-MAP2 in cells can be provided so as to detect and monitor neuroblastoma. The diagnostic agents are pairs of primers for specific amplification of DNA corresponding to at least part
OS	OS Homo sapiens.		CC	of the MAP2 transcript, provided neither primer binds to a sequence downstream of nucleotide 4168 or upstream of nucleotide 4510 of the present 5.5 kb sequence, or the corresponding antisense sequence, an oligonucleotide that binds to NB-MAP2-specific mRNA or the corresponding
PN	W0530766-A1.		CC	DNA in which nucleotides 4168 and 4510 are next to one another, an antibody specific for an epitope generated by translation of the region comprising the splice junction of NB-MAP2 specific mRNA, and a cDNA probe obtained by nick-translation or random priming of DNA or RNA specific for NB-MAP2 and obtainable from tissue or cell probes. The primers are used to detect MAP2-specific dimorphisms in tissue and cells by polymerase chain reaction (PCR) analysis. The oligonucleotide and the probes are used to detect NB-MAP2 specific transcripts (particularly by binding to membrane-bound mRNA) and the antibodies are used to detect NB-MAP2 in tissue and cells. Specifically these tests are used to detect neuroblastoma (or its precursor cells) and to monitor the success of bone marrow purging. The probes can detect bone marrow and lung metastases in cases where histopathological diagnosis of neuroblastoma is difficult. The oligonucleotide is used therapeutically to inhibit NB-MAP2 expression, resulting in development of neuroblastoma to normal ganglionneurons.
PD	25-MAR-1996; E01307.		CC	Sequence 1831 AA;
PF	27-MAR-1995; GB-006197.		CC	
PA	(HOFF) HOFFMANN LA ROCHE & CO AG F.		CC	
PI	Edwards PC, Harrington CR, Klug A, Roth M, Wischik CM;		CC	
DR	WPI: 96-45550/45.		CC	
PT	Assay for inhibitors of tau-tau interaction - used for identifying		CC	
PT	cpas., partic. phenothiazine cpds., for treating pathological		CC	
PT	tauric- or neurofilament aggregation		CC	
PS	Engle, 97pp; English.		CC	
CC	Detecting an agent which modulates or inhibits tau-tau protein		CC	
CC	association comprises contacting two tau proteins, distinct from each other yet capable of binding to the other and where one of the tau proteins is labelled, in the presence of the agent suspected of being capable of modulating or inhibiting tau-tau interaction.		CC	
CC	Agents identified as being modulators or inhibitors of tau-tau interaction may be used for the prophylaxis and treatment of Alzheimer's disease, motor neurone disease, Lewy body disease,		CC	
CC	Pick's disease or progressive supranuclear palsy.		CC	
SQ	Sequence 140 AA;		CC	
Query Match	31.9%; Score 733; DB 1; Length 140;		Query Match	31.1%; Score 713.5; DB 1; Length 1831;
Best Local Similarity	100.0%; Pred. No. 2.2e-44;		Best Local Similarity	36.5%; Pred. No. 1.3e-11;
Matches	140; Conservative		Matches	189; Conservative
OY	0; Mismatches 0; Indels 0; Gaps 0;		OY	73; Mismatches 137; Indels 119; Gaps 18;
QY	252 DLKKNVSKIGSTENLKHOPGGKVQIINKLDISNNSVSKCGSTDNIKRVPGGSVQIVK 311		QY	2 AEPQRQEYEMEDHAGDITYGLGDRKQO--GGYTHMQEG----DTDAGLKESLQT-P 51
Db	1 DLKKNVSKIGSTENLKHOPGGKVQIINKLDISNNSVSKCGSTDNIKRVPGGSVQIVK 60		Do	1348 ASPERE-EVALSEKYKETY-DDYKBDTETTDDSIMBDASLWDLTDODDRSINTEQETIP 1404
OY	312 PVDLKVTKCSIGNIHKPGGOVEVKSEKLDKFDRVOSKIGSLDNITHYGGGNKKI 371		QY	52 TPDGSEPGSEPSAD-----SIP---TAEDVAPIVDE---GAPGKQA 89
Db	61 PVDLKVTKCSIGNIHKPGGOVEVKSEKLDKFDRVOSKIGSLDNITHYGGGNKKI 120		Do	1405 KEEKEARERSLSLERKRKEPKFGRKRISTPERVKAKSEPSVSRDEVRRKAVYKA 1464
OY	372 EHKLTIFRENAKAKTDHGA 391		OY	90 AADPHTIPEGTAAERGIGSTDPSLDEAAGHTVORMVSKDGTGS----DDKKAK 143
Db	121 EHKLTIFRENAKAKTDHGA 140		Do	1465 EAKKTEQAHSPRKFIL-KPAIKTRPHTLSCVVRKTIAAGGESALAPSFKOAKD 1522
RESULT	9		QY	144 GADGKTKTATPQGAAP-----PGQKG-----QANATRPAKTP---- 176
W23329	W23329 standard; Protein; 1831 AA.		Do	1523 VSDGVTKSPKRSKSLPRPSLPPRPGVSSDRDENFSNLSSISSARRTRSEPIRAG 1582
AC	W23329;		QY	177 ---PARKPSS---GEPRKGSDGSGYSSPGSPGPGRSRSLPLTP---TREP 223
DT	23-MAR-1998 (first entry)		Do	1583 KGGTSPTPPTPSSTAATPGTPPSYSR---TPTGCTP-SYPRTHPTPGPKPSAIVPSE 1637
DE	Microtubule-associated protein 2 (MAP2).		QY	224 KVAVWTPPSPKSSAKSRQIATPVPMPLDKVNKGSKIGSTENLKHOPGGKVQINKL 283
KW	microtubule-associated protein 2; MAP2; neuroblastoma; human;		Do	1638 KVAVIITPPKSPGLPKQLINQPLDKVNKGSKIGSTENLKHOPGGKVQINKL 1697
OS	isoform; diagnosis; antibody; PCR primer; probe.		QY	284 LSNVQSKCGSKNDNIKRVPGGSVQIVKPVDLKVTKCSIGNIHKPGGOVEVK 343
OS	Homo sapiens.		Do	1698 LSH-----VSKCGSKNDNIKRVPGGSVQIVKPVDLKVTKCSIGNIHKPGGOVEVK 1726
KEY	location/Qualifiers		QY	344 LPDKDRVOSKIGSLDNITHYGGGNKKIETKLTRENAKAKTDGAEVYKSPVSGT 403
FT	Misc_difference 1825 /note= "encode by TGA"			
FT	Misc_difference 1830 /note= "encoded by TAG"			
FT	W052733-A1.			
PN	W052733-A1.			
PD	31-JUL-1997.			

Db 1727 LDFKEKAQAKVGSIDNAHVVPGGNVKIDSQKLNREHAKVDRHGAETITOSPGRSSVA 1786
 CC suffering from dementia e.g. Alzheimer's disease. The epitope is esp.
 QY 404 SPRILSNPSSTGSDIDWMDPQLALADEYSASLAKOGL 441
 CC isolated from patients who have recently died from Alzheimer's disease.
 Db 1787 SPRILSNPSSTGSDIDWMDPQLALADEYSASLAKOGL 1824
 CC It is used to generate monoclonal antibodies for the in vitro detection
 or diagnosis of brain/neurological diseases such as Alzheimer's disease
 or other diseases where neurofibrillary tangles are a pathological
 CC symptom.
 Sequence 106 AA;

RESULT 10
 R76937 Best Local Similarity 25.8%; Score 593; DB 1; Length 106;
 ID R76937; standard; Peptide; 112 AA.
 AC 0; Mismatches 0; Indels 0; Gaps 0;
 DT 04-DEC-1995 (first entry)
 DE PHF-tau (143-254) peptide.
 PT PHF-tau; paired helical filament tau protein; monoclonal antibody;
 KW MAb; phosphorylation; neurological disease; Alzheimer disease;
 KW cerebrospinal fluid.
 OS Homo sapiens.
 PN W09317439-A.
 PD 29-JUN-1995.
 PR 14-DEC-1994; EP-401133.
 PA 21-DEC-1993; EP-401133.
 PI (INNO-) INNOGENETICS NV.
 Van De Vorde A, Vandermeeren M, Vamechelen E;
 DR WPI; 95-240516/31.
 PT Novel monoclonal antibodies specific for abnormally phosphorylated
 paired helical filament tau protein (PHF-tau) - useful for post
 mortem or in vitro detection of neurological diseases eg. Alzheimer's
 disease.
 PT disease.
 PS Claim 1; Page 44; 57pp; English.
 CC Novel Mabs AT180 and AT270 (ICACC 92122204, 93010774) form
 immunological complexes with a phosphorylated epitope, given in
 R76937, of abnormally phosphorylated tau protein (PHF-tau). The
 Mabs are used to specifically detect PHF-tau in cerebrospinal fluid.
 Sequence 112 AA;

Query Match 25.8%; Score 593; DB 1; Length 112;
 Best Local Similarity 100.0%; Pred. No. 9.3e-35;
 Matches 112; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 PT
 QY 143 KGDADGKTKTAKTRGAAAPPQKGQANATRPAKTIKPAPKTPPSCEPPKSGDRSGYSSPES 202
 1 KGADGKTKTAKTRGAAAPPQKGQANATRPAKTIKPAPKTPPSCEPPKSGDRSGYSSPES 60
 Db 203 PGPGSRSRTPSLPTPPTREPKYAVVRTPPKSSAKRLQTAVPVMPDLK 254
 61 PGPGSRSRTPSLPTPPTREPKYAVVRTPPKSSAKRLQTAVPVMPDLK 112
 PR 03-OCT-1996.
 PT 27-MAR-1995; GB-006197.
 PR (HOFFMANN LA ROCHE & CO AG F.
 PA Edwards PC, Harrington CR, Klug A, Roth M, Wischik CM;
 PI Edwards PC, Harrington CR, Klug A, Roth M, Wischik CM;
 DR WPI; 96-45570/45.
 PT Assay for inhibitors of tau-tau interaction - used for identifying
 PT caps., partic. phenothiazine caps., for treating pathological
 PS tau-tau or neurofilament aggregation.
 CC Disclosure; PAGE 57; 97pp; English.
 PT Detecting an agent which modulates or inhibits tau-tau protein
 CC association comprises contacting two tau proteins, distinct from
 CC each other yet capable of binding to the other and where one of the
 CC tau proteins is labelled, in the presence of the agent suspected of
 CC being capable of modulating or inhibiting tau-tau interaction.
 CC Agents identified as being modulators or inhibitors of tau-tau
 CC interaction may be used for the prophylaxis and treatment of
 Alzheimer's disease, motor neurone disease, Lewy body disease,
 Pick's disease or progressive supranuclear palsy. Microtubule
 CC associated proteins share sequence similarity with the human tau
 CC protein in the tandem repeat region.
 Sequence 140 AA;

RESULT 11
 R93516 Best Local Similarity 24.0%; Score 551; DB 1; Length 140;
 ID R93516; standard; peptide; 106 AA.
 AC 0; Mismatches 0; Indels 0; Gaps 0;
 DT 20-SEP-1996 (first entry)
 DE Microtubule-associated tau protein epitope corr esp. to pos. 146-251;
 KW paired helical fibre; neurofibrillary tangle; dementia; neurological;
 KW Alzheimer's disease; monoclonal antibody; brain; pathology.
 OS Synthetic.
 PN W0930300-A1.
 PD 15-FEB-1996.
 PR 31-JUL-1995; EP03032.
 PR 29-JUL-1994; EP870131.
 PA (INNO-) INNOGENETICS NV.
 PI Van De Vorde A, Vamechelen E;
 DR WPI; 96-129318/13.
 PT Monoclonal antibodies specific for phosphorylated tau - for improved
 detection and diagnosis of e.g. Alzheimer's Disease.
 PT Claim 2; Page 32; 42pp; English.
 CC This is the amino acid of an epitope derived from the microtubule-
 associated tau protein. The phosphorylated subclass of tau protein
 CC from which this epitope originates forms a major part of the paired
 helical fibres which make up neurofibrillary tangles seen in patients

Query Match 24.0%; Score 551; DB 1; Length 106;
 Best Local Similarity 72.1%; Pred. No. 1e-31; Mismatches 17; Indels 0; Gaps 0;
 Matches 101; Conservative 22; Mismatches 17; Indels 0; Gaps 0;
 PT
 QY 252 DLKVKVSKGSTENLKHPGGKVKQINKKLDSNVSOKCSKDNTTRHVGPGGSVQIVYK 311
 1 DLKVKVSKGSTENLKHPGGKVKQINKKLDSNVSOKCSKDNTTRHVGPGGSVQIVYK 60
 Db 312 PVDLSKTTSKCGSLSGNIMHKPGQGVVKSELDKFQKRVQTSIGSNDNITHPGGNNKKI 371
 61 KIDLHVTKVSKGSLKNTRHRPGGGRVVKESVLFKERVQAVKGSLDNAHVPGGNVKI 120
 PR 372 ETHKLTFERNAKARTDNGAE 391
 DB 121 DSQKLNFREHAKRVDIGAE 140

RESULT	13
ID	W05284
AC	W05284; standard; Protein; 95 AA.
DT	20-DEC-1996 (first entry)
DE	Human tau protein core fragment.
KW	tau protein; inhibition; modulation; prophylaxis; treatment;
KW	progressive supranuclear palsy; Pick's disease.
OS	Homo sapiens.
PN	WO9630766-A1.
PD	03-OCT-1996.
PR	25-MAR-1996; E01307.
PA	(HOFER) HOFFMANN LA ROCHE & CO AG F.
PI	Edwards PC, Harrington CR, Klug A, Roth M, Wischik CM;
DR	WPI: 96-455570/45.
N-PSDB:	T30592
PT	Assay for inhibitors of tau-tau interaction - used for identifying
PT	cpd's, partic. phenothiazine cpds., for treating pathological
PT	tau-tau or neurofilament aggregation.
PS	Disclosure: Figure 22; 97pp; English.
CC	detecting an agent which modulates or inhibits tau-tau protein
CC	association comprises contacting two tau proteins, distinct from
CC	each other yet capable of binding to the other and where one of the
CC	tau proteins is labelled, in the presence of the agent suspected of
CC	being capable of modulating or inhibiting tau-tau interaction.
CC	Agents identified as being modulators or inhibitors of tau-tau
CC	interaction may be used for the prophylaxis and treatment of
CC	Alzheimer's disease, motor neurone disease, Lewy body disease,
CC	Pick's disease or progressive supranuclear palsy.
SQ	Sequence 95 AA;
Query Match	21.8%; Score 501; DB 1; Length 95;
Best Local Similarity	100.0%; Pred. No. 1 9e-28;
Matches	95; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
AC	RGAAPSGORGQANATRIPAKTPPAPKTPPPSSGSEPPKGDRSGYSSPGTGSRSRTPS 214
DR	1 RGAAAPSGORGQANATRIPAKTPPAPKTPPPSSGSEPPKGDRSGYSSPGTGSRSRTPS 60
OY	297 IKHVPGGSSVQIVKPKDLSKTSKCGSISGNTHKPGGGQVEVKSEKLFKDVRQSKIGS 356
Db	1 IKHVPGGSSVQIVKPKDLSKTSKCGSISGNTHKPGGGQVEVKSEKLFKDVRQSKIGS 60
OY	357 LDNITHVPGGGKIKHLTKTRENAKAKTDIGAE 391
Db	61 LDNITHVPGGGKIKHLTKTRENAKAKTDIGAE 95
RESULT	14
ID	R59837
AC	R59837; standard; peptide; 67 AA.
DR	04-MAR-1995 (first entry)
DE	Sequenee of human microtubule-associated protein tau.
KW	Tau protein; brain; cerebral cortex; hybridoma ECACC 92100853;
OS	Alzheimer's disease; monoclonal antibody; paired helical filament.
KW	Homo sapiens.
OS	W09413795-A.
PN	23-JUN-1994.
PF	10-DEC-1993; E03499.
PR	14-DEC-1992; EP-403403.
PA	(INNO-) INNOGENETICS NV SA.
PT	Paired helical filament (PHF) tau was partially purified from
CC	postmortem tissue, consisting mostly of grey matter from the frontal
CC	and temporal cortex obt. from Alzheimer patients. The tissue (5-10g)
CC	was homogenised with 10 vols of cold buffer (10mM Tris, 1mM EGTA,
CC	0.8M NaCl, 10% sucrose, pH 7.4). After centrifugation for 20 mins at
Query Match	15.9%; Score 364; DB 1; Length 67;
Best Local Similarity	100.0%; Pred. No. 4 4e-19;
Matches	67; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
AC	W34876; standard; Peptide; 55 AA.
DR	27-MAR-1998 (first entry)
OY	215 LPIPPTR 221
Db	61 LPIPPTR 67
RESULT	15
ID	W34876
PR	13-MAR-1997; J00804.
PA	(MTTU) MITSUBISHI CHEM CORP.
PI	Inahori K, Ishiguro K, Park J, Sato K, Uchida T;
DR	WPI: 97-470978/43.
PT	Antibody prepared using a partial peptide containing part of
PT	phosphorylated tau protein - used for detecting Alzheimer's disease
PS	Example: Page 37; 48pp; Japanese.
CC	An antibody prepared using a partial peptide containing the
CC	phosphorylated residue of the phosphorylated tau protein, e.g. the
CC	present sequence, in a paired helical filament, can be used to
CC	detect Alzheimer's disease, i.e. by detecting phosphorylated tau
CC	protein in brain extracts or tissue fragments.
SQ	Sequence 55 AA;
Query Match	11.8%; Score 270; DB 1; Length 55;
Best Local Similarity	100.0%; Pred. No. 1 2e-12;
Matches	55; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
AC	R59837
DR	04-MAR-1995 (first entry)
DE	Sequenee of human microtubule-associated protein tau.
KW	Tau protein; brain; cerebral cortex; hybridoma ECACC 92100853;
OS	Alzheimer's disease; monoclonal antibody; paired helical filament.
KW	Homo sapiens.
OS	W09413795-A.
PN	23-JUN-1994.
PF	10-DEC-1993; E03499.
PR	14-DEC-1992; EP-403403.
PA	(INNO-) INNOGENETICS NV SA.
PT	Paired helical filament (PHF) tau was partially purified from
CC	postmortem tissue, consisting mostly of grey matter from the frontal
CC	and temporal cortex obt. from Alzheimer patients. The tissue (5-10g)
CC	was homogenised with 10 vols of cold buffer (10mM Tris, 1mM EGTA,
CC	0.8M NaCl, 10% sucrose, pH 7.4). After centrifugation for 20 mins at
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Om protein - protein search, using sw model

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Sequence:

1 MAEPROFEVMDHAGDQTY.....SPQLATLADEVSASLAKQGL 441

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152396 seqs, 15329161 residues

Total number of hits satisfying chosen parameters: 152396

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Maximum Match 100%

Listing first 45 summaries

Database :

Issued_Patents_AA,*

1: /cgml_7/pctodata/1/iaa/5A_COMB_pep:*

2: /cgml_7/pctodata/1/iaa/5B_COMB_pep:*

3: /cgml_7/pctodata/1/iaa/6_COMB_pep:*

4: /cgml_7/pctodata/1/iaa/PCITS_COMB_pep:*

5: /cgml_7/pctodata/1/iaa/Backfilesl_pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No. Score Query Length DB ID

Description

Sequence 17, Appl1

Sequence 10, Appl1

Sequence 23, Appl1

Sequence 23, Appl1

Sequence 2, Appl1

Sequence 1, Appl1

Sequence 35, Appl1

Sequence 1, Appl1

RESULT 1
US-09-726-306A-17
Sequence 17, Application US/08/26306A
Patent No. 595864

GENERAL INFORMATION:

APPLICANT: van Leeuwen, Frederik Willem
APPLICANT: Burbach, Johannes Peter Henri
APPLICANT: Grosveld, Franklin G.
TITLE OF INVENTION: DIAGNOSIS METHOD AND REAGENTS
NUMBER OF SEQUENCES: 189
CORRESPONDENCE ADDRESS:
ADRESSEEE: Banner & Witcoff, Ltd.
STREET: 1 Financial Center
CITY: Boston
STATE: MA
COUNTRY: US
ZIP: 02111

COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.50 inch, 1.44 Mb storage
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WordPerfect 6.1

CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/726-306A
FILING DATE: 02-Oct-1996

PRIOR APPLICATION DATA:
APPLICATION NUMBER: GB 95/20080.4
FILING DATE: 02-Oct-1995

PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/009, 832
FILING DATE: 01-Jan-1996

ATTORNEY/AGENT INFORMATION:
NAME: Williams Ph.D., Kathleen M.
REGISTRATION NUMBER: 34,380
REFERENCE/DOCKET NUMBER: 96,048-A (3255/00784)

TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 345-9100
TELEFAX: (617) 345-9111

INFORMATION FOR SEQ ID NO: 17:
SEQUENCE CHARACTERISTICS:
LENGTH: 352 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: unknown
MOLECULE TYPE: protein

Query Match 75.6%; Score 1735.5; DB 2; Length 352;
Best Local Similarity 79.0%; Pred. No. 1.4e-123; Indels 93; Gaps 4;
Matches 350; Conservative 0; Mismatches 0; Sequence 26, Appl1
Sequence 25, Appl1
Sequence 24, Appl1
Sequence 23, Appl1
Sequence 22, Appl1
Sequence 21, Appl1
Sequence 20, Appl1
Sequence 19, Appl1
Sequence 18, Appl1
Sequence 17, Appl1
Sequence 16, Appl1
Sequence 15, Appl1
Sequence 14, Appl1
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Sequence 12, Appl1
Sequence 11, Appl1
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Sequence 9, Appl1
Sequence 8, Appl1
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Sequence 2, Appl1
Sequence 1, Appl1

Sequence 26, Appl1
Sequence 5, Appl1
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Sequence 19, Appl1
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Sequence 2, Appl1
Sequence 18, Appl1
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Sequence 17, Appl1
Sequence 16, Appl1
Sequence 15, Appl1
Sequence 14, Appl1
Sequence 13, Appl1
Sequence 12, Appl1
Sequence 11, Appl1
Sequence 5, Appl1
Sequence 6, Appl1
Sequence 126, APP
Sequence 36, Appl1

29 150 6.5 1210 4 PCT-US94-0496-26
30 146 6.4 1780 1 US-08-769309A-5
31 142 6.2 907 3 US-08-783474-2
32 142 6.2 907 4 PCT-US95-04611A-19
33 142 6.2 1057 3 US-08-9311820-4
34 140.5 6.1 478 3 US-08-155888-2
35 140.5 6.1 1706 2 US-08-459568-2
36 140.5 6.1 1706 2 US-08-399411-2
37 140.5 6.1 1706 3 US-08-516859A-2
38 140 6.1 1057 3 US-08-9311820-1
39 139.5 6.1 1442 2 US-08-316650-12
40 139.5 6.1 1442 4 PCT-US95-02251-12
41 139.5 6.1 1588 2 PCT-US93-07261-11
42 137 6.0 27 2 US-08-244951A-5
43 136.5 5.9 335 2 US-08-405175A-6
44 136.5 5.9 682 1 US-08-397633A-36
45 136.5 5.9 682 1 US-08-397633A-36

QY 1 MAEPROFEVMEEDHAGQDTYGLGDRKGDKDGGYTMH--QEGDTDAGLKESPLQTPTEDGSEE 58

Db 1 MAEPROFEVMEHAG--TYGLGDRKGDKDGGYTMHQDGTDAGLK----- 44

QY 59 PGSETSDAKSTPPTAEDVTAPLVDEGAPGKROAAQPHTEIPEGTTAEEGIGDPSLEDEA 118

Db 45 ----- 60

QY 119 AGHTQARMVSKKDGTGSDDKAKGADGKTKATPRGAAPPQKGQANTRPAKPPA 178

Db 61 AGHTQARMVSKKDGTGSDDKAKGADGKTKATPRGAAPPQKGQANTRPAKPPA 120

QY 179 PKPPSSGEPKPGDRSGYSSPSPGTPGSRSRTPSLPTREPKKAVVRTPPKSPSS 238

Db 121 PKPPSSGEPKPGDRSGYSSPSPGTPGSRSRTPSLPTREPKKAVVRTPPKSPSS 180

QY 239 AKSRLOTAPVPMDDLNKVKSKTOSTENLKHOPGGKVQINKKLDLSNVOSKGSKDNK 298

Db 181 AKSRLOTAPVPMDDLNKVKSKTOSTENLKHOPGGKVQINKKLDLSNVOSKGSKDNK 216

QY 299 HVPGGGSYQIVYKPVDSKVTSKCGSGLNIRHPGGGOEVKESEKLDKDRYVOSKGISLD 358

Db 217 ----- 352

QY 359 NTHVPGGGNKKIEHTKLTFRENAKDGHGAELIVYKSPVVSQDTSPRHLNSNVSTGSID 418

Db 270 NTHVPGGGNKKIEHTKLTFRENAKDGHGAELIVYKSPVVSQDTSPRHLNSNVSTGSID 329

QY 419 WMDSPOLATADEVSSLAKQGL 441

Db 330 WMDSPOLATADEVSSLAKQGL 352

RESULT 2
US-08-244-951A-10

Sequence 10 Application US/08244951A
Patent No. 584379

GENERAL INFORMATION:
APPLICANT: VANDERMEEREN, MARC; MERCKEN, MARC;

APPLICANT: VANMECHELEN, EUGÈNE; VAN DE VOORDE, ANDRE
TITLE OF INVENTION: MONOClonAL ANTIBODIES

TITLE OF INVENTION: DIRECTED AGAINST THE MICROTUBE-ASSOCIATED
TITLE OF INVENTION: PROTEIN TAU, HYBRIDOMAS SECRETING THESE
TITLE OF INVENTION: MONOClonAL ANTIBODIES, ANTIGEN RECOGNITION BY THESE
TITLE OF INVENTION: MONOClonAL ANTIBODIES AND THEIR APPLICATIONS

NUMBER OF SEQUENCES: 10
CORRESPONDENCE ADDRESS:
ADDRESSEE: BIERNAN & MUSERLIAN
STREET: 600 THIRD AVENUE
CITY: NEW YORK
STATE: NEW YORK
COUNTRY: USA
ZIP: 10016

COMPUTER READABLE FORM:
MEDIUM TYPE: FLOPPY DISK
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: ASCII
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/244-951A
FILING DATE: 19-JAN-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/EP93/03499
FILING DATE: 10-DEC-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: EP/92/403403.5
FILING DATE: 14-DEC-1992
ATTORNEY/AGENT INFORMATION:
NAME: CHARLES A. MUSERLIAN
REGISTRATION NUMBER: 19-683
REFERENCE/DOCKET NUMBER: 410.003A

TELECOMMUNICATION INFORMATION:

TELEPHONE: (212) 661-8000

TELEFAX: (212) 661-8002

INFORMATION FOR SEO ID NO.: 10:

SEQUENCE CHARACTERISTICS:

LENGTH: 391
TYPE: Amino Acid

STRANDEDNESS: Unknown

TOPOLOGY: Unknown

NAME/KEY: mTHMPH-tau1 fusion protein

US-08-244-951A-10

Query Match 75.6% Score 1735.5; DB 2; Length 391;
Best Local Similarity 79.0%; Pred. No. 1 5e-123; 0; Mismatches 0; Indels 93; Gaps 4;

Matches 350; Conservative 0; Sequence 1 MAEPROFEVMEEDHAGQDTYGLGDRKGDKDGGYTMH--QEGDTDAGLKESPLQTPTEDGSEE 58

Db 40 MAEPROFEVMEEDHAG--TYGLGDRKGDKDGGYTMHQDGTDAGLK----- 83

QY 59 PGSETSDAKSTPPTAEDVTAPLVDEGAPGKQIAAQPHTEIPGTABEAGIGDTPSLEDEA 118

Db 84 ----- 99

QY 119 AGHTQARMVSKKDGTGSDDKAKGADGKTKATPRGAAPPQKGQANTRPAKPPA 178

Db 100 AGHTQARMVSKKDGTGSDDKAKGADGKTKATPRGAAPPQKGQANTRPAKPPA 159

QY 179 PKTPPSGEPPKGDRGSGYSSPGSPGTPGERSRTPLPTREPKKAVVRTPPKSPSS 238

Db 160 PKTPPSGEPPKGDRGSGYSSPGSPGSPRSRSTSPLPTREPKKAVVRTPPKSPSS 219

QY 239 AKSRLOTAPVPMDDLNKVKSKTOSTENLKHOPGGKVQINKKLDLSNVOSKGSKDNK 298

Db 220 AKSRLOTAPVPMDDLNKVKSKTOSTENLKHOPGGKVQINKKLDLSNVOSKGSKDNK 255

QY 299 HVPGGGSYQIVYKPVDSKVTSKCGSGLNIRHPGGGOEVKESEKLDKDRYVOSKGISLD 358

Db 256 ----- 308

QY 359 NTHVPGGGNKKIEHTKLTFRENAKDGHGAELIVYKSPVVSQDTSPRHLNSNVSTGSID 418

Db 309 NTHVPGGGNKKIEHTKLTFRENAKDGHGAELIVYKSPVVSQDTSPRHLNSNVSTGSID 368

QY 419 WMDSPOLATADEVSSLAKQGL 441

Db 369 WMDSPOLATADEVSSLAKQGL 391

RESULT 3
US-08-389-011-23

Sequence 23 Application US/08389011
Patent No. 5861257

GENERAL INFORMATION:
APPLICANT: VANDERMEEREN, MARC; MERCKEN, MARC;

APPLICANT: VANMECHELEN, EUGÈNE; VAN DE VOORDE, ANDRE
TITLE OF INVENTION: MONOClonAL ANTIBODIES

TITLE OF INVENTION: DIRECTED AGAINST THE MICROTUBE ASSOCIATED
TITLE OF INVENTION: PROTEIN TAU, HYBRIDOMAS SECRETING THESE
TITLE OF INVENTION: MONOClonAL ANTIBODIES, ANTIGEN RECOGNITION BY THESE
TITLE OF INVENTION: MONOClonAL ANTIBODIES AND THEIR APPLICATIONS.

NUMBER OF SEQUENCES: 24
CORRESPONDENCE ADDRESS:
ADDRESSEE: BIERNAN & MUSERLIAN
STREET: 600 THIRD AVENUE
CITY: NEW YORK
STATE: NEW YORK
COUNTRY: USA
ZIP: 10016

COMPUTER READABLE FORM:
MEDIUM TYPE: FLOPPY DISK

COMPUTER: IBM PC COMPATIBLE
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: ASCII
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/389,011
 FILING DATE: 15-FEB-1995
 CLASSIFICATION: 435
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: 08/403,917
 FILING DATE: 19-JAN-1995
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: 08/403,916
 FILING DATE: 19-JAN-1995
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: 08/244,951
 FILING DATE: 13-JUN-1994
 ATTORNEY/AGENT INFORMATION:
 NAME: CHARLES A. NUSERLIAN
 REGISTRATION NUMBER: 19,683
 REFERENCE/DOCKET NUMBER: 410.003-1-CON
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (212) 661-8000
 TELEX: (212) 661-8002
 INFORMATION FOR SEQ ID NO: 23:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 391
 TYPE: Amino Acid
 STRANDEDNESS: Unknown
 TOPOLOGY: Unknown
 US-08-389-011-23

Query Match 75.6%; Score 1735.5; DB 2; Length 391;
 Best Local Similarity 79.0%; Pred. No. 1.6e-123; Matches 350; Conservative 0; Mismatches 0; Indels 93; Gaps 4;
 QY 1 MAEPROFEEVMDAGQDAGTYGIGDRKDQDGTYMH-QEGDTDAGLAEKSPLQTPTEDGSEE 58
 Db 40 MAEPROFEEVMDAG-TYGLDRKDQDGTYMHQDQEGETDAGK----- 83
 QY 59 PGSETSDAKSTPATAEDVTPALDEGAPGKQAAQPHTEIPGGTTAEGAGIDTPSLEDEA 118
 Db 84 -----AEEAGIDTPSLEDEA 99
 QY 119 AGHVTQARMVKSKDKGTDGSSDKKAKAGDKTIAKTRGAAPGQOKGOANTRIAPTPA 178
 Db 100 AGHVTQARMVKSKDKGTDGSSDKKAKAGDKTIAKTRGAAPGQOKGOANTRIAPTPA 159
 QY 179 PKTPPSGSEGEPPKGSGDAGYSSPGSPGSPGSRPSLPTPPTREPKAVVRTPPSPSS 238
 Db 160 PRTPPSGSEGPKGSGDRGQYSSPGSPGSRPSLPTTPTREPKAVVRTPPSPSS 219
 QY 239 AKSRLQATAPVPKPDALKVSKKGSTENLKHOPGGQWQIINKLDSINVOKGSPNDIK 298
 Db 220 AKSRLQATAPVPKPDALKVSKKGSTENLKHOPGGK----- 255
 QY 299 RVPGGGSVQIVKPKDLSKVSKCGSLGNHAKPGQVEVKSEKLDPKDVSQKGSLD 358
 Db 256 -----VOIVVKPKDLSKVSKCGSLGNHAKPGQVEVKSEKLDPKDVSQKGSLD 308
 QY 359 NITHVPGGGNKKTETKHTFRENAAKTDHGAEIVKSPVNTSGDTSRPLHSNVNSSTGSID 418
 Db 309 NITHVPGGGNKKTETKHTFRENAAKTDHGAEIVKSPVNTSGDTSRPLHSNVNSSTGSID 368
 QY 419 MYTDPQLATLADEVSAASLAKOGL 441
 Db 369 MYTDPQLATLADEVSAASLAKOGL 391

RESULT 4
 US-08-403-917A-23
 Sequence 23, Application US/08403917A
 ;
 GENERAL INFORMATION:
 PATENT NO. 6010913
 APPLICANT: VANDERMEEREN, MARC; MERCKEN, MARC;
 APPLICANT: VANNECHELEN, EUGENE;
 APPLICANT: VAN DE VOORDE, ANDRE
 TITLE OF INVENTION: MONOClonal antibodies
 TITLE OF INVENTION: DIRECTED AGAINST THE MICROTURULE-ASSOCIATED PROTEIN TAU, HYBRIDOMAS SECRETING THESE
 TITLE OF INVENTION: ANTIBODIES, ANTIGEN RECOGNITION BY THESE
 TITLE OF INVENTION: MONOCLONAL ANTIBODIES AND THEIR APPLICATION
 NUMBER OF SEQUENCES: 24
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: BIERMAN & NUSERLIAN
 STREET: 600 THIRD AVENUE
 CITY: NEW YORK
 STATE: NEW YORK
 COUNTRY: USA
 ZIP: 10016
 COMPUTER READABLE FORM:
 COMPUTER TYPE: FLOPPY DISK
 COMPUTER: IBM PC COMPATIBLE
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: ASCII
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/403,917A
 FILING DATE: 19-JAN-1995
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: 08/256,167
 FILING DATE: 27-JUN-1994
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: 08/244,951
 FILING DATE: 13-JUN-1994
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: PCT/EP93/03499
 FILING DATE: 10-DEC-1993
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: EP/92/403403.6
 FILING DATE: 14-DEC-1992
 ATTORNEY/AGENT INFORMATION:
 NAME: CHARLES A. NUSERLIAN
 REGISTRATION NUMBER: 19,683
 REFERENCE/DOCKET NUMBER: 410.003-1
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (212) 661-8000
 INFORMATION FOR SEQ ID NO: 23:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 391
 TYPE: Amino Acid
 STRANDEDNESS: Unknown
 TOPOLOGY: Unknown
 US-08-403-917A-23

Query Match 75.6%; Score 1735.5; DB 3; Length 391;
 Best Local Similarity 79.0%; Pred. No. 1.6e-123; Matches 350; Conservative 0; Mismatches 0; Indels 93; Gaps 4;
 QY 1 MAEPROFEEVMDAGQDAGTYGIGDRKDQDGTYMH-QEGDTDAGLAEKSPLQTPTEDGSEE 58
 Db 40 MAEPROFEEVMDAG-TYGLDRKDQDGTYMHQDQEGETDAGK----- 83
 QY 59 PGSETSDAKSTPATAEDVTPALDEGAPGKQAAQPHTEIPGGTTAEGAGIDTPSLEDEA 118
 Db 84 -----AEEAGIDTPSLEDEA 99
 QY 119 AGHVTQARMVKSKDKGTDGSSDKKAKAGDKTIAKTRGAAPGQOKGOANTRIAPTPA 178
 ;
 QY 239 AKSRLQATAPVPKPDALKVSKKGSTENLKHOPGGQWQIINKLDSINVOKGSPNDIK 298
 Db 220 AKSRLQATAPVPKPDALKVSKKGSTENLKHOPGGK----- 255
 QY 299 RVPGGGSVQIVKPKDLSKVSKCGSLGNHAKPGQVEVKSEKLDPKDVSQKGSLD 358
 Db 256 -----VOIVVKPKDLSKVSKCGSLGNHAKPGQVEVKSEKLDPKDVSQKGSLD 308
 QY 359 NITHVPGGGNKKTETKHTFRENAAKTDHGAEIVKSPVNTSGDTSRPLHSNVNSSTGSID 418
 Db 309 NITHVPGGGNKKTETKHTFRENAAKTDHGAEIVKSPVNTSGDTSRPLHSNVNSSTGSID 368
 QY 419 MYTDPQLATLADEVSAASLAKOGL 441
 Db 369 MYTDPQLATLADEVSAASLAKOGL 391

Query Match 75.6%; Score 1735.5; DB 3; Length 391;
 Best Local Similarity 79.0%; Pred. No. 1.6e-123; Matches 350; Conservative 0; Mismatches 0; Indels 93; Gaps 4;
 QY 1 MAEPROFEEVMDAGQDAGTYGIGDRKDQDGTYMH-QEGDTDAGLAEKSPLQTPTEDGSEE 58
 Db 40 MAEPROFEEVMDAG-TYGLDRKDQDGTYMHQDQEGETDAGK----- 83
 QY 59 PGSETSDAKSTPATAEDVTPALDEGAPGKQAAQPHTEIPGGTTAEGAGIDTPSLEDEA 118
 Db 84 -----AEEAGIDTPSLEDEA 99
 QY 119 AGHVTQARMVKSKDKGTDGSSDKKAKAGDKTIAKTRGAAPGQOKGOANTRIAPTPA 178

RESULT 5
 US/08-159-969-2
 Sequence 2, Application US/08159969
 Patent No. 5492812

GENERAL INFORMATION:
 APPLICANT: voorheis, Paul H.
 TITLE OF INVENTION: Diagnostic Method for Alzheimer's
 DISEASE
 NUMBER OF SEQUENCES: 2

CORRESPONDENCE ADDRESS:
 ADDRESSEE: Penile & Edmonds
 STREET: 1155 Avenue of the Americas
 CITY: New York
 STATE: New York
 COUNTRY: U.S.A.
 ZIP: 10036-2711

COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patientin Release #1.0, Version #1.25

CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/159, 969
 FILING DATE: 07/07/91
 CLASSIFICATION: 435
 PRIORITY APPLICATION DATA:
 APPLICATION NUMBER: US 07/7738, 778
 FILING DATE: 01-AUG-1991
 ATTORNEY/AGENT INFORMATION:
 NAME: Mistock, S.Leslie
 REGISTRATION NUMBER: 18,872
 REFERENCE/DOCKET NUMBER: 4697-040
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 212 790-9090
 TELEFAX: 212 869-8864/9741
 TELEX: 66141 PENNIE

SEQUENCE FOR SEQ ID NO: 2:
 INFORMATION FOR SEQ ID NO: 2:
 LENGTH: 351 amino acids
 TYPE: amino acid
 TOPOLOGY: linear
 MOLECULE TYPE: protein
 US-08-159-969-2

Query Match 25.8%; Score 593; DB 3; Length 112;
 Best Local Similarity 100.0%; Pred. No. 4.1e-38;
 Matches 112; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 239 AKSRLQTAPVPMPLKNTSKIGSTENLKHQPGGKVQINKKLDLSNVQSKCGSKDNK 298
 Db 160 PKTPSSGEPPKSGDRSGYSSPSPGTGSRSRTRPSLPTPEPKTAVVRPPKS 219
 QY 220 AKSRLQTAPVPMPLKNTSKIGSTENLKHQPGGK----- 255
 Db 299 HVPGGSVQIYKPVDSLKVTSKCGSLIGNIHKGPGGQVEVKSEKLDKDRYQSKIGLD 358
 Db 256 -----YQIVYKPVDSLKVTSKCGSLIGNIHKGPGGQVEVKSEKLDKDRYQSKIGLD 308
 QY 359 NITHPAGGGNNKKETHKLTFRENAAKTDHGAETIVKSPVSGDTSPRHLNSVNSTGSD 418
 Db 309 NITHPAGGGNNKKETHKLTFRENAAKTDHGAETIVKSPVSGDTSPRHLNSVNSTGSD 368
 QY 419 MVDSPOLATLADEVASASLAKQGL 441
 Db 369 MVDSPOLATLADEVASASLAKQGL 391

RESULT 6
 US/08-666-360-1
 Sequence 1, Application US/08666360
 Patent No. 6060024

GENERAL INFORMATION:
 APPLICANT:
 TITLE OF INVENTION: Monoclonal antibodies specific for PHF-tau, of these
 TITLE OF INVENTION: hybridomas secreting them, antigen recognition of these
 TITLE OF INVENTION: antibodies and their applications
 NUMBER OF SEQUENCES: 3

COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patientin Release #1.0, version #1.25 (EPO)

CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/666, 360
 FILING DATE:
 CLASSIFICATION: 435
 INFORMATION FOR SEQ ID NO: 1:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 112 amino acids
 TYPE: amino acid
 TOPOLOGY: linear
 MOLECULE TYPE: peptide
 US-08-666-360-1

Query Match 25.8%; Score 593; DB 3; Length 112;
 Best Local Similarity 100.0%; Pred. No. 4.1e-38;
 Matches 112; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 143 KGADGKTKTAPRGAAPPGORGQANATRIPAKTPPAKTPPKPSSGEPKSGDRSGYSSPGS 202
 Db 1 KQADGKTKTAPRGAAPPGORGQANATRIPAKTPPAKTPPKPSSGEPKSGDRSGYSSPGS 60

QY 203 PCTPGSRSRSLPLTPTRPEPKVAVRTPKPSASSAKSLQATAPVMPDLK 254
 Db 61 PCTPGSRSRSLPLTPTRPEPKVAVRTPKPSASSAKSLQATAPVMPDLK 112

Query Match 75.4%; Score 1731.5; DB 1; length 351;
 Best Local Similarity 79.0%; Pred. No. 2.8e-120;
 Matches 349; Conservative 0; Mismatches 0; Indels 93; Gaps 4;

QY 1 MAPPRQEFEVMEHDAGQDQG3TMHQDQEGPDAGK----- 44

RESULT 7

US 08-726-306A-35

SEQUENCE 35; Application US/08726306A

PATENT NO. 5958684

GENERAL INFORMATION:

APPLICANT: van Leeuwen, Frederik Willem

INVENTOR: Burbach, Johannes Peter Henri

TITLE OF INVENTION: DIAGNOSIS METHOD AND REAGENTS

NUMBER OF SEQUENCES: 189

CORRESPONDENCE ADDRESS:

ADDRESSEE: Banner & Witcoff, Ltd.

STREET: 1 Financial Center

CITY: Boston

STATE: MA

COUNTRY: US

ZIP: 02111

COMPUTER READABLE FORM:

MEDIUM TYPE: Diskette, 3.50 inch, 1.44 Mb storage

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: WordPerfect 6.1

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US 08/0726,306A

FILING DATE: 02-OCT-1996

PRIORITY APPLICATION DATA:

APPLICATION NUMBER: GB 95/20080.4

FILING DATE: 02-OCT-1995

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 60/009,832

FILING DATE: 01-JAN-1996

ATTORNEY/AGENT INFORMATION:

NAME: Williams, Ph.D., Kathleen M.

REGISTRATION NUMBER: 34,300

REFERENCE/DOCKET NUMBER: 96,048-A (3225/00784)

TELECOMMUNICATION INFORMATION:

TELEPHONE: (617) 345-9100

TELEFAX: (617) 345-9111

INFORMATION FOR SEQ ID NO: 35:

SEQUENCE CHARACTERISTICS:

LENGTH: 160 amino acids

TYPE: amino acid

STRANDEDNESS: single

TOPOLogy: unknown

MOLECULE TYPE: protein

US-08-726-306A-35

GENERAL INFORMATION:

APPLICANT: VANDENMEEREN, MARC; MERCKEN, MARC;

INVENTOR: VANMECHelen, EIGBEN, VAN DE VOORDE, ANDRE

TITLE OF INVENTION: MONOClonAL ANTIBODIES

TITLE OF INVENTION: DIRECTED AGAINST THE MICROTUBULE-ASSOCIATED PROTEIN TAU HYBRIDOMAS SECRETING THESE

TITLE OF INVENTION: ANTIBODIES, ANTIGEN RECOGNITION BY THESE MONOClonAL ANTIBODIES AND THEIR APPLICATIONS.

NUMBER OF SEQUENCES: 24

CORRESPONDENCE ADDRESS:

ADDRESSEE: BIERMAN & MUSERLIAN

STREET: 600 THIRD AVENUE

CITY: NEW YORK

STATE: NEW YORK

COUNTRY: USA

ZIP: 10016

COMPUTER READABLE FORM:

MEDIUM TYPE: FLOPPY DISK

COMPUTER: IBM PC COMPATIBLE

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: ASCII

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/389,011

FILING DATE: 15-FEB-1995

CLASSIFICATION: 435

PRIORITY APPLICATION DATA:

APPLICATION NUMBER: 08/403,917

PRIORITY APPLICATION DATA:

APPLICATION NUMBER: 08/403,916

PRIORITY APPLICATION DATA:

APPLICATION NUMBER: 08/444,951

PRIORITY APPLICATION DATA:

APPLICATION NUMBER: PCT/EP93/03499

PRIORITY APPLICATION DATA:

APPLICATION NUMBER: EP/92/403403.6

FILING DATE: 14-DEC-1992

ATTORNEY/AGENT INFORMATION:

NAME: CHARLES A. MUSERLIAN

REGISTRATION NUMBER: 19,683

REFERENCE/DOCKET NUMBER: 410.003-1-CON

TELECOMMUNICATION INFORMATION:

TELEPHONE: (212) 661-8000

TELEFAX: (212) 661-8002

INFORMATION FOR SEQ ID NO: 1:

SEQUENCE CHARACTERISTICS:

LENGTH: 67

TYPE: Amino Acid

STRANDEDNESS: Unknown

TOPOLogy: linear

US-08-309-011-1

RESULT 8

US-08-389-011-1

SEQUENCE 1; Application US/08389011

PATENT NO. 5861257

RESULT 9

US-08-403-917A-1

SEQUENCE 1; Application US/08403917A

PATENT NO. 6010913

GENERAL INFORMATION:

APPLICANT: VANDERMEEREN, MARC; MERCKEN, MARC;

APPLICANT: VANNECHELEN, EUGÉEN;

APPLICANT: VAN DE VOORDE, ANDRE

TITLE OF INVENTION: MONOCLONAL ANTIBODIES

TITLE OF INVENTION: DIRECTED AGAINST THE MICROTUBULE-ASSOCIATED

TITLE OF INVENTION: MONOCLONAL ANTIBODIES SECRETING THESE

TITLE OF INVENTION: ANTIBODIES, HYBRIDOMAS SECRETING BY THESE

TITLE OF INVENTION: MONOCLONAL ANTIBODIES AND THEIR APPLICATIONS

NUMBER OF SEQUENCES: 24

CORRESPONDENCE ADDRESS:

ADDRESSEE: BIERMAN & MUSERLIAN

STREET: 600 THIRD AVENUE

CITY: NEW YORK

STATE: NEW YORK

COUNTRY: USA

ZIP: 10016

COMPUTER READABLE FORM:

MEDIUM TYPE: FLOPPY DISK

COMPUTER: IBM PC COMPATIBLE

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: ASCII

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/403,917A

FILING DATE: 19-JAN-1995

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 08/256,167

FILING DATE: 27-JUN-1994

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 08/244,951A

FILING DATE: 13-JUN-1994

PRIOR APPLICATION DATA:

APPLICATION NUMBER: PCT/EP93/03499

FILING DATE: 10-DEC-1993

PRIOR APPLICATION DATA:

APPLICATION NUMBER: EP/92/403403.6

FILING DATE: 14-DEC-1992

ATTORNEY/AGENT INFORMATION:

NAME: CHARLES A. MUSERLIAN

REGISTRATION NUMBER: 19,683

REFERENCE/DOCKET NUMBER: 410.003-1

TELECOMMUNICATION INFORMATION:

TELEPHONE: (212) 661-8000

TELEFAX: (212) 661-8002

TELEFAX: (212) 661-8002

INFORMATION FOR SEQ ID NO: 1:

SEQUENCE CHARACTERISTICS:

LENGTH: 67

TYPE: Amino Acid

STRANDEDNESS: Unknown

TOPOLOGY: Unknown

TOPOLOGY: Unknown

FEATURE:

NAME/KEY: human tau protein 15-211

US-08-244-951A-1

Query Match 15.9%; Score 364; DB 3; Length 67;

Best Local Similarity 100.0%; Pred. No. 3.8e-21;

Matches 67; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Strandedness: Unknown

Topology: Unknown

Result 11

US-08-244-951A-1

Sequence 1, Application US/08244951A

Patent No. 5843779

GENERAL INFORMATION:

APPLICANT: VANDERMEEREN, MARC; MERCKEN, MARC;

APPLICANT: VAN DE VOORDE, ANDRE

APPLICANT: VANNECHELEN, EUGÉEN; VAN DE VOORDE, ANDRE

APPLICANT: VANNECHELEN, EUGÉEN

GENERAL INFORMATION:

APPLICANT: van Leeuwen, Frederik Willem

APPLICANT: Burbach, Johannes Peter Henri

APPLICANT: Grosveld, Franklin G.

TITLE OF INVENTION: DIAGNOSIS METHOD AND REAGENTS

NUMBER OF SEQUENCES: 189

CORRESPONDENCE ADDRESS:

ADDRESSEE: Banner & Witcoff, Ltd.

STREET: 1 Financial Center

CITY: Boston

GENERAL INFORMATION:

APPLICANT: VANDERMEEREN, MARC; MERCKEN, MARC;

APPLICANT: VANNECHELEN, EUGÉEN;

APPLICANT: VAN DE VOORDE, ANDRE

TITLE OF INVENTION: MONOCLONAL ANTIBODIES

TITLE OF INVENTION: DIRECTED AGAINST THE MICROTUBULE-ASSOCIATED

TITLE OF INVENTION: MONOCLONAL ANTIBODIES SECRETING THESE

TITLE OF INVENTION: ANTIBODIES, HYBRIDOMAS SECRETING BY THESE

TITLE OF INVENTION: MONOCLONAL ANTIBODIES AND THEIR APPLICATIONS

NUMBER OF SEQUENCES: 10

CORRESPONDENCE ADDRESS:

ADDRESSEE: BIERMAN & MUSERLIAN

STREET: 600 THIRD AVENUE

CITY: NEW YORK

STATE: NEW YORK

COUNTRY: USA

ZIP: 10016

COMPUTER READABLE FORM:

MEDIUM TYPE: FLOPPY DISK

COMPUTER: IBM PC COMPATIBLE

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: ASCII

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/244,951A

FILING DATE: 19-JAN-1995

CLASSIFICATION: 435

PRIOR APPLICATION DATA:

APPLICATION NUMBER: PCT/EP93/03499

FILING DATE: 10-DEC-1993

PRIOR APPLICATION DATA:

APPLICATION NUMBER: EP/92/403403.6

FILING DATE: 14-DEC-1992

ATTORNEY/AGENT INFORMATION:

NAME: CHARLES A. MUSERLIAN

REGISTRATION NUMBER: 19,683

REFERENCE/DOCKET NUMBER: 410.003A

TELECOMMUNICATION INFORMATION:

TELEPHONE: (212) 661-8000

TELEFAX: (212) 661-8002

INFORMATION FOR SEQ ID NO: 1:

SEQUENCE CHARACTERISTICS:

LENGTH: 67

TYPE: Amino Acid

STRANDEDNESS: Unknown

TOPOLOGY: Unknown

FEATURE:

NAME/KEY: human tau protein 15-211

US-08-244-951A-1

Query Match 14.8%; Score 339; DB 2; Length 67;

Best Local Similarity 92.5%; Pred. No. 2.9e-19;

Matches 62; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

Strandedness: Unknown

Topology: Unknown

Result 11

US-08-244-951A-1

Sequence 1, Application US/08244951A

Patent No. 5598684

GENERAL INFORMATION:

APPLICANT: van Leeuwen, Frederik Willem

APPLICANT: Burbach, Johannes Peter Henri

APPLICANT: Grosveld, Franklin G.

TITLE OF INVENTION: DIAGNOSIS METHOD AND REAGENTS

NUMBER OF SEQUENCES: 189

CORRESPONDENCE ADDRESS:

ADDRESSEE: Banner & Witcoff, Ltd.

STREET: 1 Financial Center

CITY: Boston

STATE: MA
COUNTRY: US
ZIP: 02111

COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.50 inch, 1.44 Mb storage
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WordPerfect 6.1

CURRENT APPLICATION DATA:
FILING DATE: 02-Oct-1996
APPLICATION NUMBER: US/08/725, 306A

PRIOR APPLICATION DATA:
APPLICATION NUMBER: GB 95/20080.4
FILING DATE: 02-Oct-1995

PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/009, 832
FILING DATE: 01-Jan-1996

ATTORNEY/AGENT INFORMATION:
NAME: Williams, Ph.D., Kathleen M.
REGISTRATION NUMBER: 34,380

TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 345-9100
TELEFAX: (617) 345-9111

REFERENCE/DOCKET NUMBER: 96,048-A (3255/00784)

SEQUENCE CHARACTERISTICS:
LENGTH: 40 amino acids

TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: Peptide

US-08-726-306A-65

Query Match 8.6%; Score 198; DB 2; Length 40;
Best Local Similarity 100.0%; Pred. No. 6.3e-09;
Matches 40; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 391 ETYKSPVWGDTSRHLNSVSTGSIDMVSQTLATLAD 430
DB 1 ETYKSPVWGDTSRHLNSVSTGSIDMVSQTLATLAD 40

RESULT 12
US-08-602-264A-10

Query Match 8.1%; Score 185; DB 2; Length 34;
Best Local Similarity 100.0%; Pred. No. 4.9e-08;
Matches 34; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 191 SDRSRGSSPSSPGTGSRSRPSLPPPTPK 224
DB 1 SDRSRGSSPSSPGTGSRSRPSLPPPTPK 34

RESULT 13
US-08-61-018A-10

Query Match 8.1%; Score 185; DB 2; Length 34;
Best Local Similarity 100.0%; Pred. No. 4.9e-08;
Matches 34; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 191 SDRSRGSSPSSPGTGSRSRPSLPPPTPK 224
DB 1 SDRSRGSSPSSPGTGSRSRPSLPPPTPK 34

RESULT 13
US-08-61-018A-10

Query Match 8.1%; Score 185; DB 2; Length 34;
Best Local Similarity 100.0%; Pred. No. 4.9e-08;
Matches 34; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 191 SDRSRGSSPSSPGTGSRSRPSLPPPTPK 224
DB 1 SDRSRGSSPSSPGTGSRSRPSLPPPTPK 34

GENERAL INFORMATION:
APPLICANT: AKIKIHO TAKASHIMA et al.
TITLE OF INVENTION: SCREENING METHOD FOR THERAPEUTIC AGENTS AGAINST
NUMBER OF SEQUENCES: 13

CORRESPONDENCE ADDRESS:
ADDRESSEE: WENDEROTH, LIND & PONACK
STREET: 805 Fifteenth Street, N.W., #700
CITY: Washington
COUNTRY: D.C.

ZIP: 20005

COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.5 inch,
MEDIUM TYPE: 1.44 mb
COMPUTER: IBM Compatible
OPERATING SYSTEM: MS-DOS
SOFTWARE: WordPerfect 5.1

CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/461, 018A
FILING DATE: June 5, 1995
CLASSIFICATION: 514

PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/204, 091
FILING DATE: March 2, 1994

ATTORNEY/AGENT INFORMATION:
NAME: Warren M. Cheek, Jr.
REGISTRATION NUMBER: 33, 367

TELECOMMUNICATION INFORMATION:
TELEPHONE:
TELEFAX:

INFORMATION FOR SEQ ID NO: 10:
SEQUENCE CHARACTERISTICS:
LENGTH: 34 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: Peptide

US-08-461-018A-10

Query Match 8.1%; Score 185; DB 3; Length 34;

Best Local Similarity 100.0%; Pred. No. 4.9e-08; Mismatches 0; Indels 0; Gaps 0; Db 1 SPGSPGTGSRSRTPSLPTPPTREPKVAVRT 33

Qy 191 SGDRGYSSPGSGSRTPSLPTPPTREPK 224
Db 1 SGDRGYSSPGSGSRSRTPSLPTPPTREPK 34

RESULT 14
; Sequence 2, Application US/08389011

Patent No. 5861257
GENERAL INFORMATION:
APPLICANT: VANDERMEEREN, MARC; MERCKEN, MARC;
TITLE OF INVENTION: MONOCLONAL ANTIBODIES
TITLE OF INVENTION: DIRECTED AGAINST THE MICROTUBULE-ASSOCIATED
TITLE OF INVENTION: PROTEIN TAU, HYBRIDOMAS SECRETING THESE
TITLE OF INVENTION: ANTIBODIES, ANTIGEN RECOGNITION BY THESE
TITLE OF INVENTION: MONOClonAL ANTIBODIES AND THEIR APPLICATION
NUMBER OF SEQUENCES: 24
CORRESPONDENCE ADDRESS:
ADDRESSEE: BIERMAN & MUSERLIAN
STREET: 600 THIRD AVENUE
CITY: NEW YORK
STATE: NEW YORK
COUNTRY: USA
ZIP: 10016

COMPUTER READABLE FORM:
MEDIUM TYPE: FLOPPY DISK
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: ASCII

CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/389,011
FILING DATE: 15-FEB-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/403,917
FILING DATE: 19-JAN-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/389,011
FILING DATE: 13-JUN-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/403,916
FILING DATE: 19-JAN-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/403,951
FILING DATE: 13-JUN-1994
ATTORNEY/AGENT INFORMATION:
NAME: CHARLES A. MUSERLIAN
REGISTRATION NUMBER: 19,683
REFERENCE/DOCKET NUMBER: 410.003-1-CON
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 661-8000
TELEFAX: (212) 661-8002

SEQUENCE INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 33
TYPE: Amino Acid
STRANDEDNESS: Unknown
TOPOLOGY: Unknown

US-08-389-011-2

RESULT 15
; Sequence 2, Application US/08403917A
; Patent No. 601013
GENERAL INFORMATION:
APPLICANT: VANDERMEEREN, MARC; MERCKEN, MARC;
APPLICANT: VANMECHelen, EUGEEN;
APPLICANT: VAN DE VOORDE, ANDRE
GENERAL INFORMATION:
APPLICANT: VANDEMEEREN, MARC; MERCKEN, MARC;
APPLICANT: VANMECHelen, EUGEEN;
APPLICANT: VAN DE VOORDE, ANDRE
TITLE OF INVENTION: MONOCLONAL ANTIBODIES
TITLE OF INVENTION: DIRECTED AGAINST THE MICROTUBULE-ASSOCIATED
TITLE OF INVENTION: PROTEIN TAU, HYBRIDOMAS SECRETING THESE
TITLE OF INVENTION: ANTIBODIES, ANTIGEN RECOGNITION BY THESE
TITLE OF INVENTION: MONOCLONAL ANTIBODIES AND THEIR APPLICATION
NUMBER OF SEQUENCES: 24
CORRESPONDENCE ADDRESS:
ADDRESSEE: BIERMAN & MUSERLIAN
STREET: 600 THIRD AVENUE
CITY: NEW YORK
STATE: NEW YORK
COUNTRY: USA
ZIP: 10016

COMPUTER READABLE FORM:
MEDIUM TYPE: FLOPPY DISK
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: ASCII

CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/403,917A
FILING DATE: 19-JAN-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/256,167
FILING DATE: 27-JUN-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/744,951
FILING DATE: 13-JUN-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/EP93/03499
FILING DATE: 10-DEC-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: EP/92/403403.6
FILING DATE: 14-DEC-1992
ATTORNEY/AGENT INFORMATION:
NAME: CHARLES A. MUSERLIAN
REGISTRATION NUMBER: 19,683
REFERENCE/DOCKET NUMBER: 410.003-1
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 661-8000
TELEFAX: (212) 661-8002
SEQUENCE INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 33
TYPE: Amino Acid
STRANDEDNESS: Unknown

US-08-403-917A-2

Query Match 7.6%; Score 174; DB 2; Length 33;
Best Local Similarity 100.0%; Pred. No. 3.2e-07; Mismatches 0; Indels 0; Gaps 0;
Matches 33; Conservative 0; Strandedness 0; Topology 0;

Qy 199 SPGSPGTGSRSRTPSLPTPPTREPKVAVRT 231
Db 1 SPGSPGTGSRSRTPSLPTPPTREPKVAVRT 33

Fri Sep 29 08:18:20 2000

us-09-142-613-1.rai

Gencore version 4.5
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OM protein - protein search, using sw model

Run on: September 28, 2000, 18:58:10 ; Search time 47.67 Seconds
(without alignments)
572.502 Million cell updates/sec

Title: US-09-142-613-1
perfect score: 2295
Sequence: MAERFQEFMVEDHAGQDRY.....SPOLATLADEVSASLAKQGL 441

Scoring table: BILOSM62
Gapop 10.0 , Gapext 0.5

Searched:

178050 seqs, 61884766 residues

Total number of hits satisfying chosen parameters: 178050

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database : PIR64:*

1: pir1:*

2: pir2:*

3: pir3:*

4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No. Score Query Length DB ID

Description

1	2262	98.6	441	1	ORHUT1	RESULT 1
2	2011.5	87.6	448	1	ORBOT1	microtubule-associated protein tau, long splice form - human
3	2003.5	87.3	432	2	JS0306	N-Alternate names: microtubule-binding protein tau; neurofibrillary tangle protein PaN; Contains: microtubule-associated protein tau type II; microtubule-associated protein PaC
4	1851.5	81.1	686	2	A38235	Species: Homo sapiens (man)
5	1851.5	81.1	733	2	A45501	Accession: JS0370; A30217; JN0009; S03796; S26665; S26666; S26667; S17302; A43444; R: Goedert, M.; Spillantini, M.G.; Jakes, R.; Rutherford, D.; Crowther, R.A.
6	1710.5	74.5	374	2	S46264	Neuron 3, 519-526, 1989
7	1558.5	67.9	316	1	QRHUT2	A:Title: Multiple isoforms of human microtubule-associated protein tau: sequences and A:Reference number: JS0370; MUID:90380393
8	1512.5	65.9	341	2	B28220	A:Molecule type: mRNA
9	1508.5	65.7	354	2	A28820	A:Residues: 1-441 <GO>
10	1493.5	65.1	402	1	ORBOT2	A:Note: six isoforms are found; the clone htau40 sequence is shown. Residues 45-73, 7 the clone htau24 sequence lacks inserts 1 and 2; the clone htau37 sequence lacks ins
11	1465.5	32.5	472	2	167793	R:Goedert, M.; Spillantini, M.G.; Potier, M.C.; Ulrich, J.; Crowther, R.A.
12	723	31.5	1830	2	A37981	EMBO J. 8, 393-399, 1989
13	719.5	31.4	1828	2	A40115	A:Title: Cloning and sequencing of the cDNA encoding an isoform of microtubule-associ
14	717.5	31.3	1825	2	S13507	A:Reference number: S03796; MUID:89251564
15	713.5	31.1	1824	1	QRHUT1	A:Accession: S03796
16	710	32.9	323	1	A53593	A:Molecule type: mRNA
17	546	23.8	381	2	S55375	A:Residues: 1-44-103-441 <GO3>
18	545	23.7	152	2	A3183	R:Goedert, M.; Brown, W.M.; Kosik, K.S.
19	523.5	22.8	125	2	B42206	Biochemistry 31, 10626-10633, 1992
20	481	21.5	15650	2	A40115	A:Title: Structure and novel exons of the human tau gene.
21	475	20.7	1072	2	A3127	A:Reference number: S26662; MUID:93041757
22	428.5	18.7	982	1	A53593	A:Accession: S26665
23	403.5	17.6	1224	2	T14007	A:Cross-references: EMBL:X14474; PIDN:CAA32636.1; PID:936725
24	278	12.1	242	2	T16349	A:Status: nucleic acid sequence not shown; translation not shown
25	193.5	8.4	1560	2	T02855	A:Molecule type: DNA
26	192	8.4	2187	2	T3026	A:Residues: 144-185 <AND>
27	184.5	8.0	1211	2	T42230	A:Cross-references: EMBL:61372; PID:936718
28	183.5	8.0	879	2	S70795	A:Note: the nucleotide sequence was submitted to the EMBL Data Library, August 1991
29	179	7.8	3507	2	T34513	A:Accession: S26666
						A:Status: nucleic acid sequence not shown; translation not shown

A; Molecule type: DNA
A; Residues: 187-274 <AN2>
A; Cross-references: EMBL:X61374; NID:936722; PID:936723
A; Note: the nucleotide sequence was submitted to the EMBL Data library, August 1991
A; Accession: S26662
A; Molecule type: DNA
A; Residues: 371-441 <ANW>
A; Cross-references: EMBL:X61373
A; Title: Identification of 3- and 4-repeat tau isoforms within the PHF in Alzheimer's disease
A; Accession: S17302
A; Species: preliminary
A; Molecule type: protein
A; Residues: 268-274, 306-395 <JAK>
R; Hasegawa, M.; Morishima-Kawashima, M.; Taxito, K.; Suzuki, M.; Titani, K.; Ihara, Y.
J. Biol. Chem. 267, 17047-17054, 1992
A; Title: Protein sequence and mass spectrometric analyses of tau in the Alzheimer's disease
A; Reference number: A43444; MUID:92381012
A; Molecule type: protein
A; Residues: 273-103-130-151-180; 191-254; 260-269; 275-290; 299-317; 322-340; 344-347; 354-383
A; Experimental source: Alzheimer's disease brain
C; Comment: sequence extracted from NCBI backbone (NCBIP:112039)
O; The core protein of the paired helical filament of Alzheimer's disease.
C; Genetics:
A; Gene: GDB:MAPT
A; Cross-references: GDB:119434; OMIM:157140
A; Map position: 17q21-17q21
C; Superfamily: microtubule-associated protein tau; MAP2/tau repeat homology
C; Keywords: alternative splicing; Alzheimer's disease; duplication; microtubule binding; microtubule-associated protein tau; long splice form #status predicted
F; 1-274_306-441/Product: microtubule-associated protein tau; long splice form #status predicted
F; 1-274_306-441/Product: microtubule-associated protein tau (clone htau39) #status predicted
F; 1-73_103-274_306-441/Product: microtubule-associated protein tau (clone htau34) #status predicted
F; 1-44_103-274_306-441/Product: microtubule-associated protein tau, fetal #status predicted
F; 1-44_103-441/Product: microtubule-associated protein tau type II #status predicted <MAPT>
F; 1-83_313/Domain: MAP2/tau repeat homology <MT3>
F; 34-344/Domain: MAP2/tau repeat homology <MT4>
F; 34-376/Domain: MAP2/tau repeat homology <MT4>

Query Match 98.6%; Score 2262; DB 1; Length 441;
Best Local Similarity 99.1%; Pred. No. 3.2e-109; Indels 4; Gaps 2;
Matches 439; Conservative 0; Mismatches 0; Codon 4; Peptide 2;

QY 1 MAEERQEFVEMEDHAGQDGYTLGLDRKDQGYTMH - QEGSTDAGIKESPLQIPTEDGSE 58
1 MAEERQEFVEMEDHAG - TYGLGKGRKDQGYTMHQDQEDTDAGIKESPLQIPTEDGSE 58
QY 59 PGSEETDAKSTAPTAEDVTAPLVIDGAGPKQAADPHTPEGTAAEAGIDTSLEDA 118
59 PGSETDAKSTAPTAEDVTAPLVIDGAGPKQAADPHTPEGTAAEAGIDTSLEDA 118
Db 119 AGHYTOQARAVSKSISDGDDKKKAGDKTKATPRGAAPPQGOANATRIPAKTPA 178
Db 119 AGHYTOQARAVSKSISDGDDKKKAGDKTKATPRGAAPPQGOANATRIPAKTPA 178
Db 179 PRIPSSGPCKPSDRGSGYSSPGSPGTPSRSPRLSPRPPTRPKVAVRPPKS 238
Db 179 PRIPSSGPCKPSDRGSGYSSPGSPGTPSRSPRLSPRPPTRPKVAVRPPKS 238
QY 239 AKSLQQTARVPMPLKVNKGSKIGSTENLHQPGGKVQINKIDLSNQSKGSKDNK 298
QY 239 AKSLQQTARVPMPLKVNKGSKIGSTENLHQPGGKVQINKIDLSNQSKGSKDNK 298
Db 299 HVPGGSVIVVYKPVDPDKLVSFTKCGSLGNHHRKPGGGQYEVKERKLDFDRVOSKIGSD 358
Db 299 HVPGGSVIVVYKPVDPDKLVSFTKCGSLGNHHRKPGGGQYEVKERKLDFDRVOSKIGSD 358

RESULT 2
ORBIT 2
microtubule-associated protein tau, form 1 - bovine
N; Contains: microtubule associated protein tau, form 2
C; Species: Bos primigenius taurinus (cattle)
C; Date: 30-Sep-1992 #sequence-revision 30-Jul-1992 #text-change 22-Jun-1999
C; Accession: A31939; A33914; S04055; R28173; B3734
R; Hämmerle, A.; Drechsler, D.; Kirschner, M.W.; Martin Jr., D.W.
Mol. Cell. Biol. 9, 1301-1318, 1989
A; Title: Tau consists of a set of proteins with repeated C-terminal microtubule-binding domains
A; Reference number: A31939; MUID:89261765
A; Accession: A31939
A; Molecule type: mRNA
A; Residues: 1-448 <HIM>
A; Cross-references: GB:N26157; NID:9114913; PID:AAA30770.1; PID:9514314
R; Iqbal, K.; Grundke-Iqbali, I.; Smith, A.J.; George, L.; Tung, Y.C.; Zaidi, T.
Proc. Natl. Acad. Sci. U.S.A. 86, 5656-5660, 1989
A; Title: Identification and localization of a tau-peptide to paired helical filaments
A; Reference number: A33914; MUID:89315854
A; Accession: A33914
A; Molecule type: Protein
A; Residues: 28, 'A', 30-38, 'IC', 41, 'AP', 44, 'LK' <IQB>
A; Experimental source: brain
A; Note: 40-Pro was also found
R; Iqbal, K.; Smith, A.J.; Zaidi, T.; Grundke-Iqbali, I.
FEBS Lett. 248, 87-91, 1989
A; Title: Microtubule-associated protein tau. Identification of a novel peptide from b
A; Reference number: S04005; MUID:89252057
A; Accession: S04005
A; Molecule type: protein
A; Residues: 28, 'A', 30-38, 'IC', 41, 'AP', 44, 'LK' <IQ2>
A; Experimental source: brain
A; Note: 40-Pro was also found
R; Paudel, H.K.; Lew, J.; Ali, Z.; Wang, J.H.
J. Biol. Chem. 268, 23512-23518, 1993
A; Title: Brain proline-directed protein kinase phosphorylates tau on sites that are a
A; Reference number: A48885; MUID:9403150
A; Accession: A48885
A; Molecule type: protein
A; Residues: 'X', '203-208, 'X', '210-211, 'X', '213-216; 238-241, 'X', '243-247, 'X', '404-410, 'X', 4
A; Experimental source: brain
A; Note: sequence modified after extraction from NCBI backbone
R; Alzeta, H.; Kawasaki, H.; Murofushi, H.; Kotani, S.; Suzuki, K.; Sakai, H.
J. Biol. Chem. 263, 7703-7707, 1988
A; Title: Microtubule-binding domain of tau proteins
A; Reference number: A28173; MUID:88227970
A; Accession: A28173
A; Molecule type: protein
A; Residues: 205-218, 'X', '220-223 <AI2>
A; Experimental source: brain
A; Cross-references: A28173; MUID:88227970
A; Molecule type: protein
A; Superfamily: microtubule-associated protein tau; MAP2/tau repeat homology
C; Keywords: alternative splicing; microtubule binding; phosphoprotein; tandem repeat
F; 1-44/Product: microtubule-associated protein tau, form 1 #status Predicted <MT3>
F; 1-174_193-448/Product: microtubule-associated protein tau, form 2 #status Predicted
F; 259-289/Region: microtubule binding #status experimental
F; 259-289/Domain: MAP2/tau repeat homology <MT1>
F; 281-320/Domain: MAP2/tau repeat homology <MT3>
F; 352-393/Domain: MAP2/tau repeat homology <MT4>
F; 202,242,248_441/Binding site: phosphate (Ser) (covalent) (by proline-directed kinase) #status e
F; 212/Binding site: phosphate (Thr) (covalent) (by proline-directed kinase) #status e

Query Match 87.6%; Score 2011.5; DB 1; Length 448;

Best Local Similarity 52.4%; Pred. No. 2.1e-86; Mismatches 22; Indels 318; Gaps 6; Matches 391; Conservative 15; Mismatches 22; Indels 318; Gaps 6;	
QY 125 -----	Db 168 QPLGTRPVEDVERSHPASELLWQESEPOKEAWGKDRLSEEVEDITDESSQESPPSQAS 227
QY 125 -----	Db 228 LARGTATPQARSVSASGVGETTSIPOFFPAEGSIPLPADFFSKVSAETQASPPPEGPGT 287
QY 125 -----	Db 348 DKQPAAGLPGRVSPRVPQLKARVAGSKDRTGNDERAKAGDKGKAKTPTRGAATPGQ 407
QY 163 KGQANATRIPAKTPPKTPSSGEPKSGDRSGYSSPGSPGTGSRSLPPTPTE 222	Db 408 KGTNSNATRIPAKTIPSPKPPGSEPPRSKGERSGTSSPGSPGTGSRSLPPTPTE 467
QY 125 -----	Db 223 PKKVAVYRTPKSPSSAKSRIQATPPMPDLKVNKXKGISTENLKIQPGGKVQINKK 282
QY 468 PKKVAVYRTPKSPSSAKSRIQATPPMPDLKVNKXKGISTENLKIQPGGKVQINKK 527	Db 283 DLNVQSKCGSKDNIKHVPGGGSVQIVYKPVLDLSKVTSCCSIGNIHHKPGGGQEVKSE 342
QY 528 DLNVQSKCGSKDNIKHVPGGGSVQIVYKPVLDLSKVTSCCSIGNIHHKPGGGQEVKSE 587	Db 343 KLDKFDRVQSKRIGSLDNITHYVPGGGNKIETHKLFRRENAAKTDHGAETIVKSPVSGD 402
QY 588 KLDKFDRVQSKRIGSLDNITHYVPGGGNKIETHKLFRRENAAKTDHGAETIVKSPVSGD 647	Db 403 TSPRKHLNSVNSTGSTIDMVDSPOLATLADEVASLASQGL 441
Db 648 TSPRLHSNSVNSTGSTIDMVDSPOLATLADEVASLASQGL 686	Db 408 PATSKRHVSSVTPRNGSPTKQMLKGADGKGAKTPTRGAASPAQKGTSPATRPPKT 467
RESULT 5	Db 168 SELNRGGPKEGMCDRLGSEEEDTVDSSQDPPSQASLTPGRAPQAGGSVC 227
A45301	Db 288 STPKSQQDLEGATWVGVPGEBOKAQTOGPSPVGKGTKEASLQEPGKQPAAGLPGRCPVSYRVP 347
MICROTUBULE-associated protein tau - mouse	Db 348 QLKARVASKDRTGNDERAKTSTPSCKAKSPHRPLSPTRPLGSSPLIKSPASPE 407
C;Species: Mus musculus (house mouse)	Db 343 QLKARVASKDRTGNDERAKTSTPSCKAKSPHRPLSPTRPLGSSPLIKSPASPE 175
C;Date: 17-Feb-1994 #sequence_revision 17-Feb-1994 #text_change 13-Aug-1999	Db 408 PATSKRHVSSVTPRNGSPTKQMLKGADGKGAKTPTRGAASPAQKGTSPATRPPKT 142
C;Accession: A45301; S31058	Db 468 QLKARVASKDRTGNDERAKTSTPSCKAKSPHRPLSPTRPLGSSPLIKSPASPE 130
R;Couchie, D.; Mayilia, C.; Georgioff, I.S.; Liem, R.K.; Shalanski, M.L.; Nunez, J.	Db 468 TSPSKTPGSGEPKRSKGERSGYSSPGSPGTGSRSLPPTPTE 527
PROC. NATL. ACAD. SCI. U.S.A., 89, 4378-4381, 1992	Db 528 PSASKSRLQTAPVMPDLKVNKXKGISTENLKIQPGGKVQINKKDLNSVQSKCGSKD 295
A;Title: Primary structure of a high molecular weight tau present in the peripheral nervous system	Db 528 PSASKSRLQTAPVMPDLKVNKXKGISTENLKIQPGGKVQINKKDLNSVQSKCGSKD 587
A;Reference number: A45301; MUID:92262443	Db 296 NIKHVPGGGSVQIVYKPVLDLSKVTSCCSIGNIHHKPGGGQEVKSKLDFKDRVQSKIG 355
A;Accession: A45301	Db 588 NIKHVPGGGSVQIVYKPVLDLSKVTSCCSIGNIHHKPGGGQEVKSKLDFKDRVQSKIG 647
A;Status: preliminary	Db 356 SLDNITHYVPGGGNKIETHKLFRRENAAKTDHGAETIVKSPVSGSTSPLRNLNSVSTG 415
A;Molecule type: mRNA	Db 648 SLDNITHYVPGGGNKIETHKLFRRENAAKTDHGAETIVKSPVSGSTSPLRNLNSVSTG 707
A;Residues: 1-33 <S0U>	Db 416 SIDMVDSPOLATLADEVASLASQGL 441
A;Note: this sequence is inconsistent with the nucleotide translation	Db 708 SIDMVDSPOLATLADEVASLASQGL 733
R;Keimer, L.; Forstner, M.; Hutter, H.; Hoefer, G.; Kurzbauer, R.; Zatloukal, K.; Krist	RESULT 6
R;Submitted to the EMBL Data Library, May 1992	S46264 microtubule-associated protein - rat
R;Reference number: S31658	C;Species: Rattus norvegicus (Norway rat)
R;Accession: S46264	C;Date: 27-Jan-1995 #sequence_revision 27-Jan-1995 #text_change 13-Aug-1999
C;Keywords: microtubule-associated protein tau; tandem repeat homology	C;Accession: S46264
C;Superfamily: microtubule-associated protein tau; MAP2/tau repeat homology	R;Sodot, E.; Marx, R.; Barg, J.; Behar, L.; Ginzburg, I.
C;Cross-references: EMBL:Z12133; NID:954253; PIDN:CAA78121_1; PID:9388534	J. Mol. Biol. 241, 325-331, 1994
C;Superfamily: microtubule-associated protein tau; MAP2/tau repeat homology	A;Title: Complete sequence of 3'-untranslated region of tau from rat central nervous
F;54-574/Domain: MAP2/tau repeat homology <NT1>	A;Reference number: S46264; MUID:94334997
F;575-605/Domain: MAP2/tau repeat homology <NT2>	A;Accession: S46264
F;636-668/Domain: MAP2/tau repeat homology <NT3>	A;Status: preliminary
F;677-687/Domain: MAP2/tau repeat homology <NT4>	A;Molecule type: mRNA
A;Residues: 1-374 <SAD>	A;Residues: 1-374 <SAD>

Db 257 LDDITAVPGGGNKKIETHLTRENAKTDHGAIEIVYKSPVSGDTSPRHLNSSTGS 316
 Qy 417 IDMDSPQLATLADEVASASLAKQGL 441
 Db 317 IDMDSPQLATLADEVASASLAKQGL 341

RESULT 9

A28820 microtubule-associated protein tau type 1 - mouse
 C;Species: Mus musculus (house mouse)
 C;Date: 30-Jun-1989 #sequence_revision 30-Jun-1989 #text_change 13-Aug-1999
 C;Accession: A28820
 R;Lee, G.; Cowan, N.; Kirschner, M.
 Science 239, 285-288, 1988
 A;Title: The primary structure and heterogeneity of tau protein from mouse brain.
 A;Reference number: A94298; MUID:88099510
 A;Accession: A28820
 A;Molecule type: mRNA
 A;Residues: 1-364 <LLE>
 A;Cross-references: GB: M18776; NID:920116; PID:AAA0166.1; PID:920117
 C;Superfamily: microtubule-associated protein tau; MAP2/tau repeat homology
 C;Keywords: alternative splicing; microtubule binding; tandem repeat
 F;183-213/Domain: MAP2/tau repeat homology <MT1>
 F;214-244/Domain: MAP2/tau repeat homology <MT2>
 F;245-276/Domain: MAP2/tau repeat homology <MT3>

Query Match 65.7%; Score 1508; DB 2; Length 364;
 Matches 309; Conservative 14; Mismatches 13; Indels 108; Gaps 6;

Qy 1 MAEPQEFEYEDHAGQDTYGLGDRKDQGYTM-M-HQEGDTAGLKEASPLQTPTEDGEE 58
 Db 1 MADPQEFDIMEDHAGD-----YLLODQEGMDHGLR----- 33
 Qy 59 PGESETDAKSTPTAEDVTAPIVDEGAPKGKAQHTEIFEGTREEAEGDTSLEDEA 118
 Db 34 -----AEEAGIGDTNQEDA 49

Query Match 65.1%; Score 1493; DB 1; Length 402;
 Best Local Similarity 79.7%; Pred. No. 6.7e-70;
 Matches 303; Conservative 14; Mismatches 29; Indels 34; Gaps 6;

Qy 119 AGHVTQARMVSKSKGAGSDKAKAGADGT-KATPRGAAPPQGQANTRIAPKT 176
 Db 50 AGHVTQARVA-SKORTGNDEKAKAGADGTGAK-TATPROGAASPAQKGTSNATRIPAKT 107
 Qy 177 PAPKTPPSSEPPKGDRGDSYSSPSRGPTGGRSRTSPLSTPPTRPEPKVAYWRPPKSP 236
 Db 108 PSKTPPPGSGEPPKSGERSGYSSPGSPGTPGSRSLPPTPTREPKVAVVRPPKSP 167
 Qy 237 SSASKRLQTAPVPMDDLNKVKSKIGSTENIKHQPGGKVQINKKDLNSVQSKCGSKDN 296
 Db 168 SASKRLOTAPEVPMDDLNKVKSKIGSTENIKHQPGGKVQINKKDLNSVQSKCGSKDN 205
 Qy 297 IKHVPGGGSYQIVVYKPVDSKVTSKCGSLGNINHHPGGGOVEVSEKLDKFRYQSKIGS 356
 Db 206 -----VQIVVYKPVDSKVTSKCGSLGNINHHPGGGOVEVSEKLDKFRYQSKIGS 256
 Qy 357 LDNITHYPGSGNKKIETHKLTRENAKTDHGAIEIVYKSPVSGDTSPRHLNSSTGS 416
 Db 257 LDNITHYPGSGNKKIETHKLTRENAKTDHGAIEIVYKSPVSGDTSPRHLNSSTGS 316
 Qy 417 IDMDSPQLATLADEVASASLAKQG 440
 Db 317 IDMDSPQLATLADEVASASLAKQGL 340

RESULT 10

QR0R22 microtubule-associated protein tau, form 3 - bovine
 N;Contains: microtubule-associated protein tau, form 4; microtubule-associated protein t
 C;Species: Bos primigenius taurus (cattle)
 C;Date: 30-Sep-1992 #sequence_revision 30-Sep-1992 #text_change 31-Mar-1996
 C;Accession: B31939; A48885; A28173

R;Himmler, A.; Drechsel, D.; Kirschner, M.W.; Martin Jr., D.W.
 Mol. Cell. Biol. 9, 1381-1388, 1989
 A;Title: Tau consists of a set of proteins with repeated C-terminal microtubule-bind
 A;Reference number: A31939; MUID:89261765
 A;Accession: B31939
 A;Molecule type: mRNA
 A;Residues: 1-402 <RIM>
 A;Cross-references: GB: M26157; GB: M26158
 J. Biol. Chem. 268, 23512-23518, 1993
 A;Title: Brain proline-directed protein kinase phosphorylates tau on sites that are e
 A;Reference number: A48885; MUID:94043150
 A;Accession: A48885
 A;Residues: 'X', 157-162, 'X', 164-165, 'X', 167-170, 192-195, 'X', 197-201, 'X', 358-364, 'X', 3
 A;Experimental source: brain
 A;Note: sequence modified after extraction from NCBI backbone
 R;Aizawa, H.; Kawasaki, H.; Murayoshi, H.; Kotani, S.; Suzuki, K.; Sakai, H.
 J. Biol. Chem. 263, 7703-7707, 1988
 A;Title: Microtubule-binding domain of Tau proteins.
 A;Reference number: A28173; MUID:88227970
 A;Accession: A28173
 A;Molecule type: protein
 A;Residues: 159-172, 'X', 174-177 <Alz>
 A;Experimental source: brain
 C;Superfamily: microtubule-associated protein tau; MAP2/tau repeat homology
 C;Keywords: alternative splicing; microtubule binding; phosphoprotein; tandem repeat
 F;1-402/Product: microtubule-associated protein tau, form 3 #status predicted <SP4>
 F;1-402/Product: microtubule-associated protein tau, form 3 #status predicted <BT7>
 F;1-402/Product: microtubule-associated protein tau, form 4 #status predicted <BT7>
 F;1-402/Region: microtubule binding #status experimental
 F;213-243/Domain: MAP2/tau repeat homology <MT1>
 F;244-274/Domain: MAP2/tau repeat homology <MT2>
 F;274-305/Domain: MAP2/tau repeat homology <MT3>
 F;306-337/Domain: MAP2/tau repeat homology <MT4>
 F;156-163, 196-202, 365/Binding site: phosphate (Ser) (covalent) (by proline-directed kinase) #status F
 F;165/Binding site: phosphate (Thr) (covalent) (by proline-directed kinase) #status F

Query Match 65.1%; Score 1493; DB 1; Length 402;
 Best Local Similarity 79.7%; Pred. No. 6.7e-70;
 Matches 303; Conservative 14; Mismatches 29; Indels 34; Gaps 6;

Qy 64 SDAKSTPTAEDVTAPIVDEGAPKGQAAQPHTEPIEGTTAERAGIGDTPLSLEDEAAGHT 123
 Db 55 SPKRPTPGSSD--PLIKRSSP-----AVCPERSSSP-----HVS 87

Qy 124 QARNVSKSKDGTSDDKRKAGDK-TKIAATPRGAAAPPQGQANTRIAPKTPTPKP 181
 Db 88 S--VTPRTGNGNSGAKRMVKRGADGKGPTKTRGAAAPPQGQANTRIAPKTPTPKT 144

Qy 182 PPSSGEPPPSGDSGQSSPSGSPOTPGSRSSRTSLSLPTPTREPKVAVTRPKPSAKS 241
 Db 145 SP--GESKGSGDGSQGSSPSGSPRSTSRLPTPTREPKVAVTRPKPSAKS 202

Qy 242 RLQATAPVNPDPDKVKVKSKIGSTENIKHQPGGKVQINKKDLNSVQSKCGSKDNKRV 301

Db 203 RLQATAPVNPDPDKVKVKSKIGSTENIKHQPGGKVQINKKDLNSVQSKCGSKDNKRV 262

Qy 302 GGGSVQIVKPVDSLKVSKCGSLGNINHHPGGGOVEVSEKLDKFRYQSKIGS 361

Db 263 GGGSVQIVKPVDSLKVSKCGSLGNINHHPGGGOVEVSEKLDKFRYQSKIGS 322

Qy 362 HVPGGGNKKIETHKLTRENAKTDHGAIEIVYKSPVSGDTSPRHLNSSTGS 421

Db 323 HVPGGGNKKIETHKLTRENAKTDHGAIEIVYKSPVSGDTSPRHLNSSTGSIDMV 382

Qy 422 SPQLATLADEVASASLAKQG 441

Db 383 SPQLATLADEVASASLAKQGL 402

RESULT 11

Db 1707 ----- -VTSKCGSLKNTRRPGGRVKLESVKLDFKEKAQKV 1743
 Qy 355 GSDLNNTTHVPGGNKRKIEHTKLTFRENKARTDHRAEIVYKSPVYSGDTSPRHNSVST 414
 Db 1744 GSDLNAHRYFGGNKIKDSOKLNFFEHAKARVDHAEITQSPSSVASPRRUSNVSS 1803
 Qy 415 GSIDMVDSPOLATLADEVSASLAKQGL 441
 Db 1804 GSINLIESPOLATLAEDVTAAKQGL 1830

RESULT 13
 A40115 microtubule-associated protein MAP2 - mouse
 N; Alternate names: MAP2
 C; Species: Mus musculus (house mouse)
 C; Date: 27-Mar-1992 #sequence_revision 27-Mar-1992 #text_change 13-Aug-1999
 C; Accession: A40115; S00467
 R; Lewis, S. A.; Wang, D.; Cowan, N. J.
 Science 242, 936-936, 1988
 A; Title: Microtubule-associated protein MAP2 shares a microtubule binding motif with tau
 A; Accession: A40115; MUID:89043973
 A; Status: preliminary
 A; Residues: 11828 <LEW>
 A; Cross-references: GB:W01041; NID:9199022; PIDN:AAA39490.1; PID:9199023
 R; Wang, D.; Lewis, S. A.; Cowan, N. J.
 Nucleic Acids Res. 16, 11369-11370, 1988
 A; Title: Complete sequence of a cDNA encoding mouse MAP2.
 A; Accession: S00467; MUID:89083571
 A; Status: translation not shown
 A; Residues: 1-1828 <WAN>
 A; Molecule type: mRNA
 C; Superfamily: microtubule-associated protein MAP2b; MAP2/tau repeat homology
 C; Keywords: microtubule binding; tandem repeat homology <MT1>
 F; 1667-1977/domain: MAP2/tau repeat homology <MT1>
 F; 1698-1728/domain: MAP2/tau repeat homology <MT2>
 F; 1729-1760/domain: MAP2/tau repeat homology <MT3>

Query Match 31.4%; Score 719.5; DB 2; Length 1828;
 Best Local Similarity 39.6%; Pred. No. 1.7e-29; Matches 176; Conservative 61; Mismatches 113; Indels 95; Gaps 13;
 Matches 176; Conservative 61; Mismatches 113; Indels 95; Gaps 13;

Qy 44 KESLQTT-----PTEGSEPESETSAKSIPTAEDVAPL----VDESGPKQKA 90
 Db 1429 KERPKFKGRISTPERVKAKESTVSDEYRKAVVKAELAKKSEVOAHSSRSRKL 1488
 Qy 91 AQPHTE-----IPEGTTAEAGIGDPSLDEAAGHVTQARMVSKDKGTGSDKK 141
 Db 1489 LKPAKIVTRPHTSCVKRKTATSGEQAQSAFKQAKDKYT-----DGT 1533

Query Match 31.3%; Score 717.5; DB 2; Length 1825;
 Best Local Similarity 39.2%; Pred. No. 1.7e-29; Matches 175; Conservative 65; Mismatches 109; Indels 97; Gaps 13;
 Matches 175; Conservative 65; Mismatches 109; Indels 97; Gaps 13;

Qy 44 KESLQTT-----PTEGSEPESETSAKSIPTAEDVAPL----VDESGPKQKA 90
 Db 1534 TKSPEKRSSLPRPSSILPQQRGVGSDREENSLSNNSISSARRTS-EPIRRAGSGT 1591
 Qy 198 SSQGSPG---IPGS----RSKTPSLTPPT--REP-----KIVAWVTPPKS 235
 Db 1592 STPITPGSTATPGTPPSYSSTPGTPGTPSYPRTGTPKGIVLPYSEKVKAIIRPKS 1651
 Qy 236 PSSAKSQTAPVMPDLKVNKSKIGSTEENLHQPGGKVKOTINKLDSLNVQSKGSKD 295
 Db 1652 PATPK-QLRINQPLDNLKNTVKSKIGTDNIKQPKGGQVQIVTKDLSH----- 1701
 Db 1492 LKPAKIVTRPHTSCVKRKTATSGDIAAPGAFQAKDVTG--ISSPERSSLRP 1549
 Qy 137 -----SDDIKAKGDKGKTKATPRGAA-----PPGQGQANAPIRTPPPARK 180
 Db 1550 SSLPQRRGVSGDRBENSFLNSNS----S:SSARRTTSEPIRRAKGSTSTPT-TPOSTAITPG 1608
 Qy 181 TPRSGEPEPKSGDGSYSS--PGFPTGSPRSRSPSLPPTRP--KXAVVTPPPSP 236
 Db 1609 TPRS-----YSSRTPCGPGPPT-SYPRRPGTPRSGIYVPSERKVAILRTPPSP 1655
 Qy 237 SSAKSRLQTAAPVMPDLKVNKSKIGSTENLKHQPGGKVQIINKLDSLNVQSKGSKD 296
 Db 1655 ATPR-QLRINQPLDNLKNTVKSKIGTDNIKQPKGGQVQIVTKDLSH----- 1704
 Db 297 IKHYPGGGSVQIVVYKPVDSLKVTSKCGSGNIIHKPGGGOVEVKSEKLFKDROSCKG 356
 Db 1705 -----VTSKCGSKLNIRHRPGGGRKVIESVKLDFKEKAQKVGS 1743
 Qy 357 LDNITHVPGGNKIKETHKLTERENAKATDHAELIVKSYKSPVYSGDTSPRHLSNVSSG 416

RESULT 14
 S13507 microtubule-associated protein MAP2 - rat
 C; Species: Rattus norvegicus (Norway rat)
 C; Accession: S13507
 R; Marchal, D.; Delapierre, D.; Dresse, A.
 Arch. Int. Physiol. Biochim. 96, 231-236, 1988
 A; Title: Cloning and partial sequencing of a new rat brain specific cDNA.
 A; Reference number: S13507; MUID:8934524
 A; Accession: S13507
 A; Status: nucleic acid sequence not shown; translation not shown
 A; Molecule type: mRNA
 A; Cross-references: EMBL:X51100; PIDN:CAA38034.1; PID:95625
 A; Note: the nucleotide sequence was submitted to the EMBL Data Library, July 1990
 C; Superfamily: microtubule-associated protein MAP2b; MAP2/tau repeat homology
 C; Keywords: microtubule binding; tandem repeat homology <MT1>
 F; 1667-1977/domain: MAP2/tau repeat homology <MT1>
 F; 1698-1728/domain: MAP2/tau repeat homology <MT2>
 F; 1729-1760/domain: MAP2/tau repeat homology <MT3>

Query Match 31.3%; Score 717.5; DB 2; Length 1825;
 Best Local Similarity 39.2%; Pred. No. 1.7e-29; Matches 175; Conservative 65; Mismatches 109; Indels 97; Gaps 13;

Qy 44 KESLQTT-----PTEGSEPESETSAKSIPTAEDVAPL----VDESGPKQKA 90
 Db 1429 KERPKFKGRISTPERVKAKESTVSDEYRKAVVKAELAKKSEVOAHSSRSRKL 1488
 Qy 91 AQPHTE-----IPEGTTAEAGIGDPSLDEAAGHVTQARMVSKDKGTGSDKK 141
 Db 1489 LKPAKIVTRPHTSCVKRKTATSGEQAQSAFKQAKDKYT-----DGT 1533

Query Match 31.3%; Score 717.5; DB 2; Length 1825;
 Best Local Similarity 39.2%; Pred. No. 1.7e-29; Matches 175; Conservative 65; Mismatches 109; Indels 97; Gaps 13;

Qy 44 KESLQTT-----PTEGSEPESETSAKSIPTAEDVAPL----VDESGPKQKA 90
 Db 1534 TKSPEKRSSLPRPSSILPQQRGVGSDREENSLSNNSISSARRTS-EPIRRAGSGT 1591
 Qy 198 SSQGSPG---IPGS----RSKTPSLTPPT--REP-----KIVAWVTPPKS 235
 Db 1592 STPITPGSTATPGTPPSYSSTPGTPGTPSYPRTGTPKGIVLPYSEKVKAIIRPKS 1651
 Qy 236 PSSAKSQTAPVMPDLKVNKSKIGSTEENLHQPGGKVKOTINKLDSLNVQSKGSKD 295
 Db 1652 PATPK-QLRINQPLDNLKNTVKSKIGTDNIKQPKGGQVQIVTKDLSH----- 1701
 Db 1492 LKPAKIVTRPHTSCVKRKTATSGDIAAPGAFQAKDVTG--ISSPERSSLRP 1549
 Qy 137 -----SDDIKAKGDKGKTKATPRGAA-----PPGQGQANAPIRTPPPARK 180
 Db 1550 SSLPQRRGVSGDRBENSFLNSNS----S:SSARRTTSEPIRRAKGSTSTPT-TPOSTAITPG 1608
 Qy 181 TPRSGEPEPKSGDGSYSS--PGFPTGSPRSRSPSLPPTRP--KXAVVTPPPSP 236
 Db 1609 TPRS-----YSSRTPCGPGPPT-SYPRRPGTPRSGIYVPSERKVAILRTPPSP 1655
 Qy 237 SSAKSRLQTAAPVMPDLKVNKSKIGSTENLKHQPGGKVQIINKLDSLNVQSKGSKD 296
 Db 1655 ATPR-QLRINQPLDNLKNTVKSKIGTDNIKQPKGGQVQIVTKDLSH----- 1704
 Db 297 IKHYPGGGSVQIVVYKPVDSLKVTSKCGSGNIIHKPGGGOVEVKSEKLFKDROSCKG 356
 Db 1705 -----VTSKCGSKLNIRHRPGGGRKVIESVKLDFKEKAQKVGS 1743
 Qy 357 LDNITHVPGGNKIKETHKLTERENAKATDHAELIVKSYKSPVYSGDTSPRHLSNVSSG 416

RESULT 15
 RHDH-----VTSKCGSKLNIRHRPGGGRKVIESVKLDFKEKAQKVGS 1743

microtubule-associated protein 2, splice form MAP-2b - human
 N; Alternate names: MAP2
 C; Species: Homo sapiens (man)
 C; Date: 31-Mar-1989 #sequence_revision 12-Apr-1996 #text_change 22-Jun-1999

A;Accession: I53693; A61085; PL0024; S34131
 R;Albata, J.S.; Kalchera, N.; Sharit-Zagardo, B.
 Gene 156, 377-378, 1993
 A;Title: Characterization of the transcripts encoding two isoforms of human microtubule-
 A;Reference number: I53693; MVID:94124038
 A;Accession: I53693
 A;Molecule type: mRNA
 A;Residues: 1-1824 <ALB>
 A;Cross-references: EMBL:Z21958; GB:L12563; NID:9348216; PID:9348218
 R;Dammann, M.; Yen, S.H.; Shafit-Zagardo, B.
 J. Neurochem. Res. 24, 487-495, 1989
 A;Title: Sequence of a human MAP-2 region sharing epitopes with Alzheimer neurofibrillary
 A;Accession: A61085; NID:90096190
 A;Status: not compared with conceptual translation
 A;Molecule type: mRNA
 A;Residues: 77-645 <DAM>
 R;Kosik, K.S.; Oreccio, L.D.; Bakalis, S.; Duffy, L.; Neve, R.L.
 J. Neurochem. 51, 587-598, 1988
 A;Title: Partial sequence of MAP-2 in the region of a shared epitope with Alzheimer neuro-
 A;Reference number: PL0024; MVID:88274407
 A;Accession: PL0024
 A;Molecule type: mRNA
 A;Residues: 489-1558 <KOS>
 A;Cross-references: GB:N25665; NID:918380; PIDN AAA5552.1; PID:918381
 C;Comment: Microtubule-associated proteins are a complex group consisting of the high mo-
 they may stabilize the microtubules against depolymerization.
 C;Genetics:
 A;Gene: GDB:MAP2
 A;Cross-references: GDB:118836; OMIM:157130
 A;Map position: 2q34-2q35
 C;Superfamily: microtubule-associated protein MAP2b; MAP2/tau repeat homology
 C;Keywords: alternative splicing; microtubule binding; phosphoprotein; tandem repeat
 F:1455_1463/Region: microtubule binding #status Predicted
 F:1667_1696/Domain: MAP2/tau repeat homology <MT>
 F:1697_1727/Domain: MAP2/tau repeat homology <MT>
 F:1728_1759/Domain: MAP2/tau repeat homology <MT>
 F:657_958_1064_1250_1505_Binding site: phosphate (Thr) (covalent) #status predicted
 F:697_817_829_1320_1417_1542_1551_Binding site: phosphate (Ser) (covalent) #status predi
 F:697_817_829_1320_1417_1542_1551_Binding site: phosphate (Ser) (covalent) #status predi

 Query Match 31.1%; Score 713.5; DB 1; Length 1824;
 Best local Similarity 36.5%; Pred. No. 2.7e-29;
 Matches 189; Conservative 73; Mismatches 137; Indels 119; Gaps 18;
 QY 2 AERQEFEMEDHAGDQTGIGDRKDQ---GGYTMHQEG----DTDGAKESPLOT-P 51
 Db 1348 ASPERE-EVSEKVT---DDYKDETIDDSIMADDLWWDODDDRSIMTQLEPT 1404
 QY 52 TEGCSEEPGSETSDAK-----STP---TAEDVTPLVDE---GAPGKA 89
 Db 1405 KEEKAEEKARRSSLEKHKREKPFKTGGRISTPERKVAKKEPSTVSRDTEVRKAVYKA 1464
 QY 90 AACQHTETEPEGTAAEAGTGDTPSLEDAEAGHVTQARMVSKSKDGTG-----DDKKAK 143
 Db 1465 ELAKKTEVOAHSFSRKFL-KPAKIKTPTHLSCVKRITAAGGESALAPSFKQAKDK 1522
 QY 144 GADGKTKTATPRGAP-----PGQKG-----DANATRIPAKP----- 176
 Db 1523 VSDCVTKSEKRSSLPRPSILPRRGVRGVGDREDENSFSNSISSARRUTSERIRRAG 1582
 QY 177 ---PAPKTPSS---GPDKSGDRSGYSSPGSPGTPSSRSRTPSLPPP----TREP 223
 Db 1583 KSGNSTPTPGSTAITPGPPSTSR---TCPGPGTP-SYPRPTPCCPKSAILVPS 1637
 QY 224 KKVAVVRTPKPSRSAAKSRLQTAEVPMPLDKNVSKIGTENLKHOPGGSKVQIINKKD 283
 Db 1638 KKVAVIRTPPKSPGLTPKQLNLINQPLPDLNKVKSKIGSTDNIKQPKGGQVQIVTKID 1697
 QY 284 LSNVQSKGSKDNKHKVPGGSYQIVVKVDSLKVTSKGSGLGNTHKGKGGQEVSEK 343
 Db 1698 LSH-----VTSKGSKLNTRHRGGRTKIESK 1726

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QY 344 LDFKDRYQSKICSLDNITTHVPGGGNNKKTEFHKLJTFRENAKAKTDHGAEIYKSPVNSGDT 403
|||: :|:||||| ||||||| :|: |||: |||: |||: |||: |||: |||: |||: |||: |||: |||: |||: |
Db 1727 LDFKEKAQKAVGSDLNAHNVPGGGNNVKIDSQKLNFREREHKARVDHGAETITQSPGRSSVA 1786
QY 404 SRHLNSVNSTGSIDMVPQLATLADEVSASLAKQGL 441
|||: :|:||||| :|:||||| :|:||||| :|:||||| :|:||||| :|:||||| :|:||||| :|:|
Db 1787 SRRLNSVSSSINTLSPQLATLADEVTAAKQGL 1824

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Fri Sep 29 08:18:21 2000

us-09-142-613-1.rpr

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OM protein - protein search, using sw model

Run On: September 28, 2000, 19:59:12 ; Search time 47.83 Seconds

Total number of hits satisfying chosen parameters: 85661

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

Database : SwissProt_38:*

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 85661 seqs., 30989115 residues

Title: US-09-142-613-1

Sequence: 2295 1 MAEPROFEVEMEDHAGQDTY.....SPOUATLADEVSASLAKOGL 441

Result

No.	Score	Query	Length	DB	ID	Description
1	2262	98.6	441	1	TAU_HUMAN	P10636 homo sapien
2	2011.5	87.5	441	1	TAU_BOVIN	P29172 bos taurus
3	2003.5	87.3	432	1	TAU_RAT	P19332 rattus norv
4	1512	65.9	341	1	TAU_MOUSE	P10637 mus musculus
5	1508	65.7	364	1	TAU2_MOUSE	P10638 mus musculus
6	1493	65.1	402	1	TAU3_BOVIN	P29173 bos taurus
7	863.5	37.6	1861	1	MAP2_RAT	P15146 rattus norv
8	719.5	31.4	1827	1	MAP2_MOUSE	P20337 mus musculus
9	716	31.2	1827	1	MAP2_HUMAN	P11137 homo sapien
10	545	23.7	1152	1	MAP4_HUMAN	P27816 homo sapien
11	523.5	22.8	1125	1	MAP4_MOUSE	P27756 mus musculus
12	475	20.7	1072	1	MAP4_BOVIN	P30225 bos taurus
13	175.5	7.0	704	1	NP24_RAT	P41777 rattus norv
14	145	7.6	857	1	NFM_CHICK	P16053 gallus gallus
15	163.5	7.1	825	1	ICP0L_HSV2H	P22844 herpes simp
16	163.5	7.1	915	1	NFM_HUMAN	P01977 homo sapien
17	161.5	7.0	670	1	VG50_RSVIL	P01301 ictalurid h
18	161.5	7.0	831	1	NFH_RAT	P16884 rattus norv
19	161	7.0	3924	1	ANK2_HUMAN	Q01484 homo sapien
20	160.5	7.0	1411	1	TCP1_HUMAN	Q13422 homo sapien
21	160	7.0	1487	1	ICP4_HSVEB	P28925 equine herp
22	158.5	6.9	1367	1	AMYH_YEAST	P05640 saccharomyces
23	158	6.9	1487	1	ICP4_HSVER	P17473 equine herp
24	157	6.8	1164	1	BAG_STRAG	P21951 streptococc
25	156.5	6.8	1906	1	KMUS_CHICK	P11799 gallus gallus
26	155	6.8	699	1	VGLG_HS2V	P13290 herpes simp
27	155	6.8	1150	1	APMO_PIG	P10211 sus scrofa
28	154.5	6.7	2805	1	MARA_HUMAN	P78559 homo sapien
29	154	6.7	1446	1	IEB_PRVKA	P33479 pseudorabies
30	154	6.7	1664	1	SLPI_CLOTH	Q08852 clostridium
31	153.5	6.7	573	1	C114_MOUSE	P19467 mus musculus
32	152.5	6.7	1115	1	NCAL1_MOUSE	P13595 mus musculus
33	152	6.6	1029	1	CA26_MOUSE	Q02788 mus musculus

SUMMARIES

RESULT

NO.	TAU_HUMAN	STANDARD;	PRT;	441 AA.
AC	P10636; P18518; Q1799; Q15551;			
DT	01-JUL-1989 (Rel. 11, Created)			
DT	15-DEC-1998 (Rel. 37, Last sequence update)			
DT	15-DEC-1998 (Rel. 37, Last annotation update)			
DE	MICROTUBULE-ASSOCIATED PROTEIN TAU.			
GN	MAPT OR MBT1.			
OS	Homo sapiens (Human).			
OC	Oukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RX	Medline; 9304157.			
RA	Andreadis A., Brown W.M., Kosik K.S.;			
RT	"Structure and novel exons of the human tau gene.";			
RL	Biochemistry 31:10626-10633(1992).			
RN	[2]			
RP	SEQUENCE OF 1-44 AND 103-441 FROM N.A.			
RC	TISSUE=BRAIN;			
RC	MEDLINE; 89251564.			
RA	Goedert M., Spillantini M.G., Potier M.C., Ulrich J., Crowther R.A.;			
RT	"Cloning and sequencing of the cDNA encoding an isoform of microtubule-associated protein tau containing four tandem repeats: differential expression of tau protein mRNAs in human brain.";			
RT	EMBO J. 8:393-399(1989).			
RL	[3]			
RP	SEQUENCE OF 1-26 AND 306-441 FROM N.A.			
RC	TISSUE=BRAIN;			
RC	MEDLINE; 88234557.			
RA	Goedert M., Wischik C., Crowther R., Walker J., Klug A.;			
RT	"Cloning and sequencing of the cDNA encoding a core protein of the paired helical filament of Alzheimer disease: identification as the microtubule-associated protein tau.";			
RT	Proc. Natl. Acad. Sci. U.S.A. 85:4051-4055(1988).			
RL	[4]			
RP	SEQUENCE OF 1-26 AND 306-441 FROM N.A.			
RC	TISSUE=BRAIN;			
RC	MEDLINE; 90180482.			
RA	Lee G., Neve R.L., Kosik K.S.;			
RT	"The microtubule binding domain of tau protein.";			
RL	Neuron 2:1615-1624(1999).			
CC	ICP0_HUMAN PROMOTES MICROTUBULE ASSEMBLY AND STABILIZES MICROTUBULES.			
CC	-- ALTERNATIVE PRODUCTS: THE DIFFERENT FORMS OF TAU SEEM TO BE PRODUCED BY ALTERNATIVE SPLICING.			
CC	-- DOMAIN: THE REPEATED DOMAIN BINDS TO TUBULIN.			
CC	-- PTM: VARIOUS SERINE RESIDUES IN THE REPEATS MAY BE PHOSPHORYLATED BY CAMP KINASE.			
CC	-- DISEASE: TAU CONSTITUTES AT LEAST A PART OF THE PAIRED HELICAL FILAMENT (PHF) CORE IN ALZHEIMER DISEASE.			
CC	-- SIMILARITY: CONTAINS 3 OR 4 TAU/MAP REPEATS.			
CC	-- DATABASE: NAME=HotMolecBase; NOTE="tau entry"; WWW="http://bioinformatics.weizmann.ac.il/hotmolecbase/entries/tau.htm".			

ALIGNMENTS

Db 257 LDNITHYPGGNNKKIETHKLTERENAKTDHGAELIVKSPVWSGDASPRHLNSVSSSGS 316
 Qy 417 IDMVSQPLATLADEVASLAKOG 440
 Db 317 IDMVSQPLATLADEVASLAKOG 340

RESULT 6
 TAU3_BOVIN STANDARD; PRT; 402 AA.
 ID P29173; 01-DEC-1992 (Rel. 24, last sequence update)
 AC DT 15-DEC-1998 (Rel. 37, last annotation update)
 DE MICROTUBULE-ASSOCIATED PROTEIN TAU FORMS 3, 4, AND 5.
 GN MAPT.
 OS Bos taurus (Bovine).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia;
 OC Bovidae; Bovinae; Bos.
 RP [1]
 RX SEQUENCE FROM N.A.
 RA Himmer A., Drechsel D., Kirschner M.W., Martin D.W. Jr.;
 RT microtubule-binding domains and variable N-terminal domains.;
 RL Mol. Cell. Biol. 9:1381-1386(1989).
 CC -I- FUNCTION: TAU PROTEIN PROMOTES MICROTUBULE ASSEMBLY AND STABILIZES
 CC MICROTUBULES.
 CC -I- ALTERNATIVE PRODUCTS: THE DIFFERENT FORMS OF TAU SEEM TO BE
 CC PRODUCED BY ALTERNATIVE SPLICING.
 CC -I- DOMAIN: THE REPEATED DOMAIN BINDS TO TUBULIN.
 CC -I- PTM: VARIOUS SERINE RESIDUES IN THE REPEATS MAY BE PHOSPHORYLATED
 CC BY CAMP KINASE.
 CC -I- SIMILARITY: CONTAINS 3 OR 4 TAU/MAP REPEATS.
 CC
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 CC
 CC DR M26158; AAA30711.; -.
 CC PRM: PR00418; tubulin-binding; 4.
 DR PRM; PR00418; tubulin-binding; 4.
 DR PRM; PR00229; TAU_MAP_1; 4.
 KW MICROTUBULE; Repeat; Alternative splicing.
 FT REPEAT . 205 235 TAU/MAP MOTIF.
 FT REPEAT . 236 266 TAU/MAP MOTIF.
 FT REPEAT . 267 297 TAU/MAP MOTIF.
 FT REPEAT . 298 329 TAU/MAP MOTIF.
 FT VARSPLIC 1 100 MISSING (IN ISOFORM 4).
 FT VARSPLIC 1 235 296 MISSING (IN ISOFORM 5).
 SO SEQUENCE 402 AA; 42232 MW; A7FCED47A04D7340 CRC64;

Query Match 65.1%; Score 1493; DB 1; Length 402;
 Best Local Similarity 79.7%; Pred. No. 7; 2a-65; Mismatches 29; Indels 34; Gaps 6;
 Matches 303; Conservative 14; Score 1493; DB 1; Length 402;
 Qy 64 SDAKSTPTAEDVTAFLPVGDEAGPKQAAQPHTEIPPESTAEEGIGDTPSLEDAAGHVT 123
 Db 55 SKRPPGSSD--PLPKPSS-----AVCPPESSSPK-----HVS 87

Qy 124 QARMVSKSKDGCGSDKKAKGADCK--TKIAAPRGAAPPGOKQAAQTRPAKTPAPKT 181
 Db 88 S---VTPRTGNNSAKEMKVKGDKPGKTIAPRGAAPPGOKQAAQTRPAKTPAPKT 144
 Qy 182 PPSSEGPXPKSGRSQYSPGSPCTPGRSRSTSLLPPTREKKVAVRTPKPSAKS 241
 Db 145 SP--GESCKSGDRSGYSSPGPCTPGSRSRSTSLLPPTREKKVAVRTPKPSAKS 202

Qy 242 RLOTAPVMPMDIKNVSKIGSTENLKHOPOGGKVQINKLDSNWQSCKCSKDNIKHVP 301
 Db 203 RQQAAPCPMPDQKVNKSIGSENLKHOPOGGKVQINKLDSNWQSCKCSKDNIKHVP 252

Qy 302 GGGSVQTVKPKPDLSKVTSKCGSLGNHHKPGQQEVKSERLDFKDRVQSKLGSNDIT 361
 Db 263 GGGSVQTVKPKPDLSKVTSKCGSLGNHHKPGQQEVKSERLDFKDRVQSKLGSNDIT 322

Qy 362 HYPGGGNNKKIENHKLTRENAAKTHGAELTYKSPVWSGTSPRELSNSSTGSDIMDV 421
 Db 323 HYPGGGNNKKIENHKLTRENAAKTHGAELTYKSPVWSGTSPRELSNSSTGSDIMDV 382

Qy 422 SQPLATLADEVASLAKOGL 441
 Db 383 SQPLATLADEVASLAKOGL 402

RESULT 7
 MAP2_RAT STANDARD; PRT; 1861 AA.
 ID MAP2_RAT
 AC P15146;
 DT 01-APR-1990 (Rel. 14, Created)
 DT 01-JUN-1994 (Rel. 29, Last sequence update)
 DT 01-OCT-1994 (Rel. 30, Last annotation update)
 DE MICROTUBULE-ASSOCIATED PROTEIN 2 (MAP2B) [CONTAINS: MAP2C].
 GN MAP2.
 OS Rattus norvegicus (Rat).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
 RP [1]
 RN SEQUENCE OF 1-1694 AND 1726-1861 FROM N.A.
 RC STRAIN=WISTAR; TISSUE=BRAIN;
 RX MEDLINE: 9051471.
 RA Kindle S., Schwake B., Schulz B., Garner C.C.;
 RT "Complete cDNA sequence encoding rat high and low molecular weight
 MAP2.";
 RL Nucleic Acids Res. 18:2822-2822(1990).
 RN [2]
 RP SEQUENCE OF 1-1694 AND 1726-1861 FROM N.A.
 RC STRAIN=WISTAR; TISSUE=BRAIN;
 RX MEDLINE: 91060576.
 RA Kindle S., Schulz B., Goedert M., Garner C.C.;
 RT "Molecular structure of microtubule-associated protein 2b and 2c from
 rat brain.;"
 J. Biol. Chem. 265:19679-19684(1990).
 RN [3]
 RP SEQUENCE OF 1-151; 1515-1694 AND 1726-1861 FROM N.A.
 RX MEDLINE: 9021819.
 RA Doll T., Papandikopoulou A., Matus A.;
 RT "Nucleotide and amino acid sequences of embryonic rat MAP2c.";
 RL Nucleic Acids Res. 18:361-361(1990).
 RN [4]
 RP DISCUSSION OF SEQUENCE.
 RX MEDLINE: 89365159.
 RA Papandikopoulou A., Doll T., Tucker R.P., Garner C.C., Matus A.;
 RT "Embryonic MAP2 lacks the cross-linking sidearm sequences and
 dendritic targeting signal of adult MAP2.";
 RL Nature 340:650-652(1989).
 RN [5]
 RP SEQUENCE OF 1695-1725 FROM N.A.
 RX MEDLINE: 91110302.
 RA Doll T., Meichsner M., Riederer B.M., Honegger P., Matus A.;
 RT "An isoform of microtubule-associated protein 2 (MAP2) containing
 four repeats of the tubulin-binding motif.";
 RL J. Cell. Sci. 106:633-640(1993).
 CC -I- FUNCTION: THE EXACT FUNCTION OF MAP2 IS UNKNOWN BUT MAPS MAY
 CC STABILIZE THE MICROTUBULES AGAINST DEPOLIMERIZATION. THEY ALSO
 CC SEEM TO HAVE A STIFFENING EFFECT ON MICROTUBULES.
 CC -I- ALTERNATIVE PRODUCTS: VARIOUS FORMS OF MAP2 ARE PRODUCED BY
 CC ALTERNATIVE SPLICING OF THE SAME GENE. MAP2C, THE LOW MOLECULAR
 CC FORM OF MAP2, LACKS THE CENTRAL DOMAIN OF MAP2A/B.
 CC -I- DEVELOPMENTAL STAGE: MAP2C IS EXPRESSED DURING EMBRYONIC BRAIN

CC DEVELOPMENT AND UNTIL POSTANATAL DAY 10. MAP2B IS EXPRESSED
CC THROUGHOUT BRAIN DEVELOPMENT.
CC -!- SIMILARITY: CONTAINS 3 OR 4 TAU/MAP REPEATS.

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CC

DR X51842; CAA36135.1; -
DR EMBL; X17682; CAA36667.1; -
DR EMBL; X11487; CAA0588.1; -
DR PIR; S07887; S10003; S1003;
DR PIR; A37981; A37981;
DR PROSITE; PS00229; TAU_MAP_1;
DR MICROTUBULE; Repeat; Alternative splicing; Calmodulin-binding.
FT DOMAIN 1654 1474 CALMODULIN-BINDING (POTENTIAL).
FT REPEAT 1664 1694 TAU/MAP MOTIF.
FT REPEAT 1695 1725 TAU/MAP MOTIF.
FT REPEAT 1726 1756 TAU/MAP MOTIF.
FT VARSPlic 152 1514 MISSING (IN ISOFORM MAP2C).
FT VARSPlic 1695 1725 MISSING (IN ISOFORM WITH 3 TAU/MAP REPEATS).
FT SEQUENCE 1861 AA; 202409 MW; 42DCF116D21EF54 CRC64;

Query Match 37.6%; Score 863.5; DB 1; Length 1861;
Best Local Similarity 44.3%; Pred. No. 2.7e-34; Mismatches 115; Indels 67; Gaps 12;
Matches 188; Conservative 67; CC

QY 44 KESPLQT-----PREDGSSEPGSETSDAKSTPTAEDVTHPLVDG----APGKQA 89
Db 1433 KERPKFGGRGRITPERREVAKKEPSTYRSDEVRKKAVYKKAELAKESEVQAHSPRKL 1492

QY 90 AAPHTE-----IPEGTAAEAGIGDTTPSLEDEAGHVVQARMVSKSKCGTGSDK 140
Db 1493 ILKPAIKTRPTHLSCVKRKTTATSGESAQAPSFKQAKDVKT-----DG 1537

QY 141 KAGADGKTIKATPRGAAPP-GOKG-QANATIPIAKTPPKTPPSGEPPKGDRSG 196
Db 1538 ITSPPEKKSSLPRPSSILPQQSGDRREENSSLSNISSSARRTRS-EPIRRAGSG 1595

QY 197 YSSPGSPG---IPGS---RSRPSLPLPPPT--REP-----KKVWWRTPK 234
Db 1596 TSPTTPGSTAITPGTPSYSSRPTPGTPGTPSPRTPKSGTILVPSSEKKVAILRTPK 1655

QY 235 SPSSAKSLQTAQVPMPLDKNVSKIGSTEENLKHQPGGKVQINKKDLSNWSQSKGSK 294
Db 1656 SPATPK-OLRLINQPLPDLKVNVSIGSTDNKIQPKQGVRTLINKKHDPSKVSRCGSK 1714

QY 295 DNTRKHVPGGGSVQIVYKPVDSLKVTSKGSLGNITHKPGGGQVQINKKDLSNWSQSKGSK 354
Db 1715 DNTHKSAGGGNVOVTKKIDSVTTSKQSKLNIRHRGGGRKYESKLDFFEKAOQVY 1774

QY 355 GSDNITIHYPGGGNKKIETHKLFPRENAKTHQAGAEIVYKSPVVSQDTSPRILNSYST 414
Db 1775 GSIDNAHHHVPGGGNVKIDSQKLNFREHAKARDHGAEITOSPSRSSVASPRLLSNVSS 1834

QY 415 GSDMWDSPOLATLADEVASASLKGGL 441
Db 1835 GSINLLESPOLATAEDVTAALKQGL 1861

CC

DR PIR; A37981; tubulin-binding; 4.
DR PROSITE; PS00229; TAU_MAP_1;
DR MICROTUBULE; Repeat; Alternative splicing; Calmodulin-binding.
FT DOMAIN 1654 1474 CALMODULIN-BINDING (POTENTIAL).
FT REPEAT 1664 1694 TAU/MAP MOTIF.
FT REPEAT 1695 1725 TAU/MAP MOTIF.
FT VARSPlic 152 1514 MISSING (IN ISOFORM MAP2C).
FT VARSPlic 1695 1725 MISSING (IN ISOFORM WITH 3 TAU/MAP REPEATS).
FT SEQUENCE 1861 AA; 202409 MW; 42DCF116D21EF54 CRC64;

Query Match 31.4%; Score 719.5; DB 1; Length 1828;
Best Local Similarity 39.6%; Pred. No. 1.8e-27; Mismatches 113; Indels 95; Gaps 13;
Matches 176; Conservative 61; CC

QY 44 KESPLQT-----PREDGSSEPGSETSDAKSTPTAEDVTHPLVDG----VDEGAPGKQA 90
Db 1432 KERPKFGGRGRITPERREVAKKEPSTYRSDEVRKKAVYKKAELAKESEVQAHSPRKL 1491

QY 91 AAPHTE-----IPEGTAAEAGIGDTTPSLEDEAGHVVQARMVSKSKCGTGDKG---- 136
Db 1492 ILKPAIKTRPTHLSCVKRKTTATSGESAQAPSFKQAKDVKT-----ISKSPERKSSLPP 159

QY 137 -----SDDKKGARGAERTKATPRGA-----PPGOKGQANATHIPIAKTPPKP 180
Db 1550 SSLPSPRGVGSDREENSSLSNISSSARRTRSEPIRRAKGSGTSTPT-TPGSTAIFG 1608

QY 181 TPSSGPRPKSDRSYTS--PGSCTPGCRSRSLPLTPPTRED--KKVWWRTPK 236
Db 1609 TPBS-----YSSPGSPG---RSRPSLPLPPPT--REP-----KKVWWRTPK 1655

QY 237 SSAKSLQTAQVPMPLDKNVSKIGSTEENLKHQPGGKVQINKKDLSNWSQSKGSK 296
Db 1656 ATPK-OLRLINQPLPDLKVNVSIGSTDNKIQPKQGVRTLINKKHDPSKVSRCGSK 1704

QY 297 IKHPGGGSVQIVYKPVDSLKVTSKGSLGNITHKPGGGQEVKSEKLDKDRV3KIGS 356

RESULT 8
MAP2_MOUSE STANDARD; PRT: 1828 AA.
ID MAP2_MOUSE AC P20357;

FT	CONFFLICT	9	9	A -> G (IN REF. 2).
FT	CONFLICT	37	37	R -> A (IN REF. 2).
FT	CONFLICT	108	108	A -> G (IN REF. 2).
FT	CONFLICT	152	155	MISSING (IN REF. 2).
FT	CONFLICT	187	187	S -> K (IN REF. 2).
FT	CONFLICT	1655	1655	A -> GL (IN REF. 2).
FT	SEQUENCE	1736	1736	V -> A (IN REF. 2).
DB	1705	-----VTKCGSLKNIRHRPGGRVRIESKUDREKAQVG	1743	
QY	357	LDNITHPGGGNNKIEHKLTRENAAKTDHGAEIYVKSWSVSGTSRPRILNSVSTGS	416	
FT	1744	LDNAHYPGNGVNVKIDSQKLNFRHAKARVNDGAELITOSPRSSVAVSPRRLNSVSSGS	1803	
QY	417	IDMVDSPOLLADAEVSASLAKOGL	441	
DB	1804	INLIESPQLATLAEVDTAALAKOGL	1828	
Query Match		31.2%	Score 716;	DB 1;
Best Local Similarity		36.9%	Pred. No. 2.	7e-27;
Matches		191;	Conservative	75;
			Mismatches	132;
			Indels	120;
			Gaps	19;
QY	2	AEPRFEEVMEDHAGCDTYGLGDKDQ--GGYTMHQEG----DTAGLKEPLQT-P	51	
AC	: :	: : : : :	:	
DT	01-JUL-1989 (Rel. 11, Created)			
DT	01-JUN-1994 (Rel. 29, Last sequence update)			
DT	15-JUL-1999 (Rel. 38, Last annotation update)			
DE	MICROTUBULE-ASSOCIATED PROTEIN 2 (MAP2B) [CONTAINS: MAP2C].			
GN				
OS	Homo sapiens (Human).			
OC	Bukarrotta; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.			
NN	[1] SEQUENCE FROM N.A.			
RP	Price R.;			
RA	Submitted (SEP-1993) to the EMBL/GenBank/DDJB databases.			
RL	[2]			
RN	SEQUENCE FROM N.A., AND ALTERNATIVE SPlicing.			
RC	TISSUE-BRAIN;			
RX	MEDLINE: 9412408.			
RA	Albalia J.S., Kalcheva N., Shafit-Zagardo B.;			
RR	*Characterization of the transcripts encoding two isoforms of human			
RT	microtubule-associated protein-2 (MAP-2).*			
RL	J. Neurochem. 51:587-598(1988).			
CC	-1- FUNCTION: THE EXACT FUNCTION OF MAP2 IS UNKNOWN BUT MAPS MAY			
CC	STABILIZE THE MICROTUBULES AGAINST DEPOLARIZATION. THEY ALSO			
CC	SEEM TO HAVE A STIFFENING EFFECT ON MICROTUBULES.			
CC	-1- ALTERNATIVE PRODUCTS: VARIOUS FORMS OF MAP2 ARE PRODUCED BY			
CC	ANALYTICAL FORM OF MAP2, LACKS THE CENTRAL DOMAIN OF MAP2A/B.			
CC	-1- SIMILARITY: CONTAINS 3 TAU/MAP REPEATS.			
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DR	EMBL; U01828; AAA0354_1; -			
DR	EMBL; U89350; AAB48088_1; -			
DR	EMBL; M2568; AAA59552_1; -			
DR	PIR; P10024; QHOMT.			
DR	MIM; 157130; -			
DR	PFAM; PF00418; tubulin-binding; 3.			
DR	PROSITE; PS00229; TAU_MAP_1; 2.			
KW	Microtubules; Repeat; Alternative splicing; Calmodulin-binding.			
FT	DOMAIN; 1447 1467 CALMODULIN-BINDING (POTENTIAL).			
FT	REPEAT; 1661 1691 TAU/MAP MOTIF.			
FT	REPEAT; 1692 1722 TAU/MAP MOTIF.			
FT	REPEAT; 1723 1754 TAU/MAP MOTIF.			
FT	VARSPPLIC 152 1507 MISSING (IN ISOFORM MAP2C).			
RESULT	9			
MAP4_HUMAN				
ID				
AC	MAP4_HUMAN	STANDARD;	PRT;	1152 AA.
DT	01-AUG-1992 (Rel. 23, Created)			
DT	01-AUG-1992 (Rel. 23, Last sequence update)			
DT	01-JUN-1994 (Rel. 29, Last annotation update)			
DE	MICROTUBULE-ASSOCIATED PROTEIN 4.			
GN				
OS	Homo sapiens (Human).			
OC	Bukarrotta; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.			
RN	[1] SEQUENCE FROM N.A.			
RX	MEDLINE: 92042100.			
RA	West R.R., Tenbarge K.M., Olmsted J.B.;			
RT	*A model for microtubule-associated protein 4 structure. Domains			
RT	defined by comparisons of human, mouse, and bovine sequences.;			
RL	J. Biol. Chem. 266:21886-21895(1991).			
RN	[2] SEQUENCE OF 102-1152 FROM N.A.			
RC	TISSUE-BRAIN;			

Query Match 22.8%; Score 523.5; DB 1; Length 1125;
 Best Local Similarity 33.9%; Pred. No. 2.3e-18;
 Matches 149; Conservative 51; Mismatches 128; Indels 11; Gaps 14;

QY 44 KESPIQTPIEDGSEERGSEEDANSTPTAEDVTPALVDEGAPGKQAAQP-HTEIPEGT 102
 Db 625 KETPOSQRSPCGSVSROEAKAAGVGTVNDITPPNKEPPSPKARPLATOPAKMS 584
 QY 103 AEEA-----GIGDTP---SLEDBAUGHTQARNSKSKDT-GSDD 139
 Db 685 TSKARTQPTSLPKPAPPTSGGLNKPKMSLASGVPAAHKRPAATAATRSPHLRDY 744
 QY 140 K----KAKGADGKTKIATPRG--AAPPGQR-----GQANATRIPAKT-P 176
 Db 745 KPKPITEAKVAEKRISPSKESADLSPKALPGPKTPTVSKATSPSTIVLNGPSSRATLIP 804
 QY 177 PAPKPPSSGEP-----PKSGPSSGSSPGSGTGPSSRSPSLPPP-----TR--- 221
 Db 805 KRPTSIKTECKPADVKRMKTAKSASDLSRSKTSAASSVRNTPTGAAPPAGMTSTRVKP 864
 QY 222 --EPKVVAVRIPPKSPSSAK-----SRLQTPAVPMPDLUKWKSKIGSTEINLKHPG 271
 Db 865 MSASRSSEALSVDKPTSPKPTSPKSSAPRVSLATT-VSAPDLKSVRSKVKGSTEINKHQPQ 923
 QY 272 G-----GKVOQTINKKUDLSNYOKGGS 293
 Db 924 GGRAKVEKKEATTAGKPEPNATKAAGSIASASKQPKPAGKVQIVSKVSYHSIQSCVS 983
 QY 294 KDNTRKHVPGGSYOIVVYKPVDSLKTSKGSLGMINHKGGGGCOTEYKEBKLDKDRVOSK 353
 Db 984 KDNIKHVPGCGNVQIQNKVDISKVSSKGSKANKKHKGDDVRIESEOKLNFKRQAQK 1043
 QY 354 IGSIDNITHVPGGNKIE 372
 Db 1044 VGSLLDNVGHFPAGCAVTE 1062

RESULT 12

MAP4_BOVIN STANDARD: PRT: 1072 AA.

ID MAP4_BOVIN AC P36225; DT 01-JUN-1994 (Rel. 29, Created, Last sequence update) DE MICROTUBULE-ASSOCIATED PROTEIN 4 (MICROTUBULE-ASSOCIATED PROTEIN-U) (MAP-U) OS Bos taurus (Bovine); Chordata; Craniata; Vertebrata; Buteleostomi; Eukaryote; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi; OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae; Bovidae; Bovinae; Bos. RN [1] RP SEQUENCE FROM N.A., AND PARTIAL SEQUENCE. RX MEDLINE_9033002. RA Aizawa H., Emori Y., Murofushi H., Kawasaki H., Sakai H., RA Suzuki K.; RT "Molecular cloning of a ubiquitously distributed microtubule-associated protein with Mr 190,000."; RT J. Biol. Chem. 265:13849-13855(1990). RN [2] DOMAINS. RX MEDLINE_91236765. RA Aizawa H., Emori Y., Mori A., Murofushi H., Sakai H., Suzuki K.; RT Functional analyses of the domain structure of microtubule-associated protein-4 (MAP-U)."; RT J. Biol. Chem. 266:9841-9846(1991). CC -I- FUNCTION: NON-NEURONAL MICROTUBULE-ASSOCIATED PROTEIN. PROMOTES MICROTUBULE ASSEMBLY. CC -I- TISSUE SPECIFICITY: IS DISTRIBUTED UNIQUITUOUSLY AMONG ALL TISSUES BUT AMOUNTS ARE LOWER IN CEREBELLUM AND LIVER. CC -I- PTM: PHOSPHORYLATION OF THE PRO-RICH REGION IN THE C-TERMINUS NEGATIVELY REGULATES MAP-4 ACTIVITY TO PROMOTE MICROTUBULE ASSEMBLY.

CC -I- SIMILARITY: CONTAINS 3 TAU/MAP REPEATS.

CC -----
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CC -----
 DR EMBL; D01419; BAA14179_1; PIR; A37127; A37127.
 DR PFAM; PF00418; tubulin-binding; 3.
 DR PROSITE; PS00229; TAU_MAP_1; 3.
 KW MICROTUBULES; Repeat; Phosphorylation.
 FT DOMAIN 244 530 19 X 14 AA TANDEM REPEATS.
 FT REPEAT 244 257 1.
 FT REPEAT 258 271 2.
 FT REPEAT 272 285 3.
 FT REPEAT 286 299 4.
 FT REPEAT 300 313 5.
 FT REPEAT 314 327 6.
 FT REPEAT 328 341 7.
 FT REPEAT 342 355 8.
 FT REPEAT 384 391 9. (INCOMPLETE).
 FT REPEAT 392 405 10.
 FT REPEAT 406 417 11.
 FT REPEAT 418 431 12.
 FT REPEAT 432 445 13.
 FT REPEAT 446 460 14.
 FT REPEAT 461 474 15.
 FT REPEAT 475 488 16.
 FT REPEAT 489 502 17.
 FT REPEAT 503 516 18.
 FT REPEAT 517 530 19.
 FT REPEAT 537 557 20.
 FT REPEAT 561 581 21.
 FT REPEAT 597 617 22.
 FT REPEAT 638 658 23.
 FT REPEAT 669 689 24.
 FT REPEAT 938 958 25.
 FT REPEAT 969 1000 26.
 SQ SEQUENCE 1072 AA; 111914 MW; E8C17A730989FD02 CRC64;

Query Match 20.7%; Score 475; DB 1; Length 1072;
 Best Local Similarity 31.7%; Pred. No. 4.4e-16; Mismatches 125; Conservative 53; Indels 128; Gaps 20;

QY 32 TMHOEGDTDAKIGESP-----LOPTDENDS-----BEPGSESTDAYKSTPTADEV 75
 Db 558 SLQDEGQSAVPLMTSPERWVANGQKHSPLTDSDVLEBLQKPKSSQTSSELSETSG--V 615
 QY 76 TAPLVDEGAP-----GKPAAPRHPELTPEGTAEAGGDPDPSLEDAAGHTQARNSV 130
 Db 616 AKP--EEGPPTGSVSGNDITAPPKELPPSPRKTPKPLATTOPAKTSTSAKTQPTSLPK 673
 QY 131 SKGQT--GSDDKAKGDKTKIATPRGAGPKQGANA--TRPAK--TPPAP--K 180
 Db 674 QTAPTTLGNSKPKMSTASGSP-----AAPKPKPAATSPSPSTPSKDKTPKPKVPEAK 727
 QY 181 TP-----PSSGEPPKSGDGSYSSPGSPG-----PGSSRSRTPSLPTP--PT----- 220
 Db 728 IPEKRVFSKPKASAPAVPKGSSTQVPKPAPATLASPGPSRNLSTPLPRPTAKTE 787
 QY 221 --REPKVAVRTP-----PSS-----SSAKSPLQ--TAPV-----TAPV-- 249
 Db 788 GKPREKMMATSKAPDLSRKPISTTSSVKKSTVPGTAPPGAPSRAKPTAPPRPSGT 847
 QY 250 -----MDPKVNSKIGSIZENLKHQPGGGVWQVNLK 282
 QY 848 PPTDKKPTAAKPTSSAPRLGRYANASAPDLKNVRKVGSSENKHPGGERAK-YEKKT 906
 QY 283 DLS-----NYQSKGSKDNKTHVPGGSYQIVVYKVDISKVTSKCGSIGNIHKGPG 334
 Db 907 EAAPAKRPEPNAVTKAGPIQNAQKPTGKQVIONKVDISKVSSCGSKANIKRPG 966

QY	335 GOVENKESEKIDFKDORYOSKIGSLDNITHYFGGGNNKIE 372	FT DOMAIN 478 487 POLY-SER.
Db	967 GDVKIESQKLNFKEQAQTVGSLDNVHGLPAGGAVKE 1004	FT DOMAIN 521 528 POLY-GLU.
NPI1_RAT	RA "NOPP140 shuttles on tracks between nucleolus and cytoplasm.";	FT DOMAIN 567 572 POLY-GLU.
ID	P4177;	STANDARD; PRT; 704 AA.
AC	01-Nov-1995 (Rel. 32, Created)	
DT	01-Oct-1995 (Rel. 32, Last sequence update)	
DE	140 kDa NUCLEOLAR PHOSPHOPROTEIN (NOPP140).	
OS	Rattus norvegicus (Rat);	
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrates; Euteleostomi;	
OMIM	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.	
[1]		
RP	SEQUENCE FROM N.A., AND SEQUENCE OF 292-309 AND 563-601.	
RC	TISSUE=LIVER;	
RT	RX MEDLINE: 92323542.	
RA	Meier U.T.; Blobel G.;	
CC	"NOPP140 shuttles on tracks between nucleolus and cytoplasm.";	
RL	Cell 10:127-138(1992).	
CC	- !- FUNCTION: MAY FUNCTION AS A CHAPERONE FOR IMPORT INTO AND/OR FROM THE NUCLEOLUS. IT COULD FUNCTION TO COVER AND NEUTRALIZE HIGHLY CHARGED DOMAINS OF PRERIBOSOMAL PARTICLES (EXPORT) OR OF RIBOSOMAL PROTEINS (IMPORT). BINDS NUCLEAR LOCALIZATION SEQUENCES; THE BINDING TO SUCH SEQUENCES IS DEPENDENT ON PHOSPHORYLATION. THE STATE OF PHOSPHORYLATION MAY REPRESENT A MEANS OF REGULATING THE PROTEIN'S AFFINITY FOR NLS-CONTAINING PROTEINS AND THEREBY ITS ABILITY TO FUNCTION IN NUCLEOCTOPLASMIC TRANSPORT.	
CC	- !- SUBCELLULAR LOCATION: SHUTTLES ON CURVILINEAR TRACKS BETWEEN NUCLEOLUS AND CYTOPLASM. THESE TRACKS EXTEND FROM THE DENSE FIBRILLAR COMPONENT OF THE NUCLEOLUS ACROSS THE NUCLEOPLASM TO A LIMITED NUMBER OF NUCLEAR PORNE COMPLEXES.	
CC	- !- PTM: THIS PROTEIN UNDERGOES RAPID AND MASSIVE PHOSPHORYLATION AND DEPHOSPHORYLATION ON CK-2 AND PKC SITES. NOPP140 IS ONE OF THE MOST PHOSPHORYLATED PROTEINS IN THE CELL.	
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CC	- !- DR: M94287; AAA41718; -	
CC	EMBL: M94288; AAA41719; -	
CC	DR: M94287; AAA41718; -	
CC	EMBL: M94288; AAA41719; -	
CC	KW Nuclear protein; Phosphorylation; Repeat; Chaperone; Transport.	
CC	DOMAIN 84 570 Nucleic protein; Phosphorylation; Repeat; Chaperone; Transport.	
FT	REPEAT 84 95 ACIDIC SERINE CLUSTER. 1.	
FT	REPEAT 127 138 ACIDIC SERINE CLUSTER 1.	
FT	REPEAT 170 181 ACIDIC SERINE CLUSTER 2.	
FT	REPEAT 231 242 ACIDIC SERINE CLUSTER 3.	
FT	REPEAT 274 285 ACIDIC SERINE CLUSTER 4.	
FT	REPEAT 335 346 ACIDIC SERINE CLUSTER 5.	
FT	REPEAT 373 384 ACIDIC SERINE CLUSTER 6.	
FT	REPEAT 434 445 ACIDIC SERINE CLUSTER 7.	
FT	REPEAT 479 490 ACIDIC SERINE CLUSTER 8.	
FT	REPORT 524 535 ACIDIC SERINE CLUSTER 9.	
FT	REPORT 559 570 ACIDIC SERINE CLUSTER 10.	
FT	VARIANT 150 150 ACIDIC SERINE CLUSTER 11.	
FT	MOD_RES 567 567 MISSING (IN NOPP140B).	
FT	DOMAIN 126 131 PHOSPHORYLATION (BY CK2).	
FT	DOMAIN 136 140 POLY-SER.	
FT	REPORT 141 146 POLY-LYS.	
FT	DOMAIN 226 236 POLY-SER.	
FT	DOMAIN 274 277 POLY-SER.	
FT	DOMAIN 283 287 POLY-GLU.	
FT	DOMAIN 432 435 POLY-SER.	
FT	DOMAIN 439 442 POLY-SER.	
RESULT 13		
NPI1_RAT		
ID	P4177;	STANDARD; PRT; 704 AA.
AC	01-Nov-1995 (Rel. 32, Created)	
DT	01-Oct-1995 (Rel. 32, Last annotation update)	
DE	140 kDa NUCLEOLAR PHOSPHOPROTEIN (NOPP140).	
OS	Rattus norvegicus (Rat);	
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrates; Euteleostomi;	
OMIM	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.	
[1]		
RP	SEQUENCE FROM N.A., AND SEQUENCE OF 292-309 AND 563-601.	
RC	TISSUE=LIVER;	
RT	RX MEDLINE: 92323542.	
RA	Meier U.T.; Blobel G.;	
CC	"NOPP140 shuttles on tracks between nucleolus and cytoplasm.";	
RL	Cell 10:127-138(1992).	
CC	- !- FUNCTION: MAY FUNCTION AS A CHAPERONE FOR IMPORT INTO AND/OR FROM THE NUCLEOLUS. IT COULD FUNCTION TO COVER AND NEUTRALIZE HIGHLY CHARGED DOMAINS OF PRERIBOSOMAL PARTICLES (EXPORT) OR OF RIBOSOMAL PROTEINS (IMPORT). BINDS NUCLEAR LOCALIZATION SEQUENCES; THE BINDING TO SUCH SEQUENCES IS DEPENDENT ON PHOSPHORYLATION. THE STATE OF PHOSPHORYLATION MAY REPRESENT A MEANS OF REGULATING THE PROTEIN'S AFFINITY FOR NLS-CONTAINING PROTEINS AND THEREBY ITS ABILITY TO FUNCTION IN NUCLEOCTOPLASMIC TRANSPORT.	
CC	- !- SUBCELLULAR LOCATION: SHUTTLES ON CURVILINEAR TRACKS BETWEEN NUCLEOLUS AND CYTOPLASM. THESE TRACKS EXTEND FROM THE DENSE FIBRILLAR COMPONENT OF THE NUCLEOLUS ACROSS THE NUCLEOPLASM TO A LIMITED NUMBER OF NUCLEAR PORNE COMPLEXES.	
CC	- !- PTM: THIS PROTEIN UNDERGOES RAPID AND MASSIVE PHOSPHORYLATION AND DEPHOSPHORYLATION ON CK-2 AND PKC SITES. NOPP140 IS ONE OF THE MOST PHOSPHORYLATED PROTEINS IN THE CELL.	
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CC	- !- DR: M94287; AAA41718; -	
CC	EMBL: M94288; AAA41719; -	
CC	DR: M94287; AAA41718; -	
CC	EMBL: M94288; AAA41719; -	
RESULT 14		
NPI1_RAT		
ID	P4177;	STANDARD; PRT; 857 AA.
AC	P16053;	
DT	01-APR-1990 (Rel. 14, Created)	
DE	01-APR-1990 (Rel. 14, Last sequence update)	
OS	01-Oct-1996 (Rel. 34, Last annotation update)	
GN	NEUROFILAMENT TRIPLET M PROTEIN (160 kDa NEUROFILAMENT PROTEIN) (NFM).	
OC	NEUFILAMENT, METAZOA; AVES; NEognathae; Galliformes; Phasianidae; Phasianinae; Gallus gallus (Chicken).	
OC	Archosauria; Metazoa; Chordata; Craniata; Vertebrates; Euteleostomi; Gallus.	
RN	[1]	
RP	SEQUENCE FROM N.A.	
RC	RX MEDLINE: 9014973.	
RT	RA Zopf D., Dineva B., Betz H., Gundelfinger E.D.; RT "isolation of the chicken middle-molecular weight neurofilament gene and characterization of its promoter.";	
RT	RT (NF-M) gene and characterization of its promoter.	
RT	RT Nucleic Acids Res. 18:521-529(1990).	
RT	RT [2]	
RT	RT SEQUENCE OF 259-857 FROM N.A.	
RT	RT MEDLINE; 8812814.	
RT	RA Zopf D., Hermans-Borgmeyer I., Gundelfinger E.D., Betz H.; RT "Identification of gene products expressed in the developing chick visual system: characterization of a middle-molecule-weight neurofilament cDNA.";	
RT	RT Genes Dev. 1:699-708(1987).	
RT	- !- FUNCTION: NEUROFILAMENTS USUALLY CONTAIN THREE IF PROTEINS: L, M,	

CC AND H WHICH ARE INVOLVED IN THE MAINTENANCE OF NEURONAL CALIBER.
 CC -!- PTM: THERE ARE A NUMBER OF REPEATS OF THE TRIPPIEDE K-S-P, NFM IS
 CC PHOSPHORYLATED ON A NUMBER OF THE SERINES IN THIS MOTIF. IT IS
 THOUGHT THAT PHOSPHORYLATION OF NFH RESULTS IN THE FORMATION OF
 CC INTERFILAMENT CROSS BRIDGES THAT ARE IMPORTANT IN THE MAINTENANCE
 OF AXONAL CALIBER.

CC OF THE LARGER NEUROFILAMENT POLYPEPTIDES (NF-M AND NF-H), THE
 CC LEVELS OF PHOSPHORYLATION BEING ALTERED DEVELOPMENTALLY AND
 CC COINCIDENT WITH A CHANGE IN THE NEUROFILAMENT FUNCTION.

CC -!- SIMILARITY: BELONGS TO THE INTERMEDIATE FILAMENT FAMILY.

CC

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CC

CC

CC EMBL; X17102; CAA34959.1; -.

CC DR EMBL; X05558; CAA29073.1; -.

CC DR PIR; A27040; A27040.

CC DR PIR; S15762; S15762.

CC DR PROSITE; PS00226; IF; 1.

CC DR PROSITE; PS00226; IF; 1.

KW Intermediate filament; Heptad repeat pattern; Coiled coil; Neurone;

KW Phosphorylation; Glycoprotein.

FT INIT_MER 0 0

FT DOMAIN 1 98 HEAD.

FT DOMAIN 99 405 ROD.

FT DOMAIN 407 857 TAIL.

FT DOMAIN 99 130 COIL 1A.

FT DOMAIN 131 143 LINKER 1.

FT DOMAIN 144 242 COIL 1B.

FT DOMAIN 243 259 LINKER 12.

FT DOMAIN 260 281 COIL 2A.

FT DOMAIN 282 285 LINKER 2.

FT DOMAIN 286 406 COIL 2B.

FT CARBOHYD 46 426 O-LINKED (GlcNAc) (BY SIMILARITY).

FT CARBOHYD 426 546 O-LINKED (GlcNAc) (BY SIMILARITY).
 G -> R (IN REF. 2).

FT CONFLICT 546 95704 MW; 4E2E0FC6AC64778B CRC64;

SO SEQUENCE 857 AA; 95704 MW;

Query Match 7.5%; Score 175.5; DB 1; Length 857;
 Best Local Similarity 20.0%; Pred. No. 0.06; Indels 153; Gaps 14;

Matches 81; Conservative 62; Mismatches 153; Insertions 109; Gaps 14;

OY 6 QEEPEVMDHAGODTYGLGDRKDQGGYTMHQEGDTAGLKEPLQTPTEDGSEEPGSETSD 65

Db 510 EEEKEKEEEEEEAKSAASDAEEGSKKEELTEKEGEAEPEEAAGKAKGKAAEAGKVEK 569

OY 66 ARSTPTAEDVTAPLVDEGAPGQKAAQPHTEPPEGTAEEAGIGDTPSLEDAAGHTQA 125

Db 570 VPKSPAK-----SPPKSPKSPVIE-----QA 591

OY 126 RAVSKSKDGTCDDKKAKGAD-----RKTKTATPRGAAPPGQKQGQANATRI 171

Db 592 YVQKKAEEVGKDKQAKAEEKAEEKAASPEKPATPKVPSPEKPATPEKPKPTPEKATT 651

OY 172 PAK-TTPPKP-----PSSGEPKPSGDRGSGSPGPTPSRSRSPSLPPP-- 219

Db 652 PEYVRSSEKPTPEKPTPEKVSPEKKSAPSPKPTPEK-ASPERPATP-EKPRPEKATPEK 708

OY 220 TREPDKVAVRTPPKISSAKRLQTAAPVPMPLDKVSKGTSNEKMHQPGGKVQIIN 279

Db 709 PRSPKE-----PSFLKDERAKVWEISITVKVTAEVNSKARKEDIAVNGVEEE 761

OY 280 KKLDSNVOSKGSKDNKHVPGGGVQIVKPVDSKVTKGSGSIGNTHKPGCGQVE 339

Db 762 KKDEAKEKEKEEEEKG-----VTINGLDDVSPVDER-----GKRVVV 797

Query Match 7.1%; Score 163.5; DB 1; Length 825;
 Best Local Similarity 24.1%; Pred. No. 0.22; Mismatches 120; Indels 139; Gaps 18;

Matches 92; Conservative 31; Mismatches 120; Indels 139; Gaps 18;

OY 2 AEPROPEVMDHAGODTYGLGDRKDQGGYTMHQEGDT---AGLKES--PLQTPTE 53

Db 47 SEEETEGISDDDLHD-----STSEAGSTBTEMFENGMDAATPPARPPAE 93

OY 54 -DGSEBPGSTSADNSTPTAE-----DVTAPLVDSGAPGQKAAQP----- 93

Db 94 RQGSPPTPADAQGSCGGGPVGEAEAGGGDVCAVCTDETAPLRCQSFPCLHPFCIPCM 153

QY	94	RTEIPEGTTAEEAG-----IGDTPS-----LEDEAA-----1199
Db	154	KTWIPLRNTCPCLNTPVAYLIVGVTASGSFSТИPIVNDPRTVEAEAWRAGTAVIDFWT 213
Oy	120	-----GHVTOARMYSKSKGCGSDKKANGDKTKIAPRGAAPPGQGQA 166
Db	214	GNPRTADRSLSLGQTTRA-LSPTPPWPGTODDDDLADLVVPAAPR-RAPRGCGA 2700
Oy	167	NATR---IPAKTPPAPKTPP---SSGEPKGSCDRSGYSSPGSPGTGCSRSPSLP--- 216
Db	271	GATRGTSOPPAATRPAPPGAPRSSSSGGAPLRAVGVG---SSGGPAAVAVPRVLSPPA 3288
Oy	217	-TPTREEK----KAVAVTPPKPSASSKSRLQTAPEVPPM 2511
Db	329	GGGRAGAARRVGEDAAAEGRTTPARQFRAAQEPPIVSDSPPPSP---RRPAGPPLS 3831
Oy	252	DLKNVSKIGSTENLKHOPGGG 273
Db	384	FVSSSSAQVSS----GPGGG 399

Search completed: September 28, 2000, 20:03:59
Job time: 287 sec

GenCore version 4.5
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OM protein - protein search, using sw model

Run on:

September 28, 2000, 19:58:24 ; Search time 49.63 Seconds

(without alignments) 616.086 Million cell updates/sec

Title: perfect score:

US-09-142-613-1

2295 MAEPROFEVEMEDHAGDQDY.....SPOLATLADEVASASLAQQL 441

Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5

Scoring table:

Searched: 225878 seqs, 69334122 residues

Total number of hits satisfying chosen parameters: 225878

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SPREMBL12,*

- 1: SP_archea;*
- 2: SP_bacteria;*
- 3: SP_fungi;*
- 4: SP_human;*
- 5: SP_invertebrate;*
- 6: SP_mammal;*
- 7: SP_mhc;*
- 8: SP_orangutan;*
- 9: SP_phage;*
- 10: SP_plant;*
- 11: SP_primate;*
- 12: SP_virus;*
- 13: SP_vertebrate;*
- 14: SP_unclassified;*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query	Match Length	DB ID	Description
1	1993.5	86.9	430	11	060684
2	1878	81.8	402	6	005828
3	1861.5	81.5	686	11	063567
4	1770.5	74.5	374	11	003677
5	1678.5	74.0	372	11	060685
6	1678.5	72.3	416	6	028187
7	1577.5	69.2	350	11	006066
8	1524	66.4	369	6	028185
9	1415	61.7	447	6	028188
10	1410	61.4	365	6	028186
11	1337.5	58.3	338	6	028190
12	1288.5	53.5	6	028189	bos taurus
13	717.5	31.3	1825	11	004715
14	714	31.0	1828	11	003724
15	710	30.9	323	6	028869
15	690.5	30.1	198	11	P97749
17	626	27.3	124	11	028286
18	546	23.8	381	11	064710
19	545	23.7	152	4	Q13082

RESULT	1	PRELIMINARY;	PRT;	430 AA.
ID	060684			
AC	060684			
DT	01-NOV-1996 (TREMBLrel. 01, Created)			
DT	01-NOV-1996 (TREMBLrel. 01, Last sequence update)			
DE	MICROTUBULE-ASSOCIATED PROTEIN TAU ISOFORM 23.			
OS	Mus musculus (Mouse)			
OC	Eukaryota; Metazoa; Chordata; Craniata; vertebrata; Mammalia; OC			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RC	STRAIN-HIM OF1 SPF; TISSUE=LIVER;			
RA	KENNER L., EFERL R., ZATKOWSKI K., HOERLIER G., DENK H.,			
RL	Submitted (ADG-1994) to the EMBL/genBank/DBJ databases.			
DR	EMBL; U12114; AAA5843.1; -;			
DR	PROSITE; PS00229; TAU_MAP; 4;			
DR	PFAM; PF00418; tubulin-binding; 4;			
KW	MICROTUBULES; Repeat;			
SQ	SEQUENCE 430 AA; 44893 MW; FD52F5A CRC32;			

Query Match 86.9%; Score 1993.5; -DB 11; length 430;
Best Local Similarity 87.9%; Pred. No. 6.5e-119;
Matches 391; Conservative 16; Mismatches 19; Indels 19; Gaps 4;
Ov 1 MAEPROFEVEMEDHAGDQDY.....SPOLATLADEVASASLAQQL 441
Db 1 MADPROFEVEMEDHAGDQDY.....YTLQDQEGDMIDIGIKESPQPPADG 47
Ov 59 PGESETDAKSTPTAEDVTRPLVDEGAPGQQAOPRHTPEPEGTAEEAGIDFTSLEBA 118
Db 48 PGSEETDAKSTPTAEDVTRPLVDEGAPGQQAOPRHTPEPEGTAEEAGIDFTSLEBA 107
Db 119 AGHYTOARMVSKSKDGTGKAGDGT-KIATPRGAAPPGQKGOANATRIPAKTP 176
Db 108 AGHTQARVA-SKDRTGNDKEKAGDGTGKAKTPRGAAPRQGTSNATRIPAKTP 165
Ov 177 PAKKIPPSGERPISGDGSGYSPGSPGPGGSRSRTPSLPPTREPKVAVVRTPKSP 236
Db 166 PSKTPPPGSGEPKSGERGYSISPGSPGTPGSSRSRTPSLPPTREPKVAVVRTPKSP 225

QY 237 SSAKSRLQTAPVPMPLKAVNSKGSTENLKHOPGGKVQIINKLDSNVQSKGSNDN 296
 :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
 FT MOD-RES 223 223 BY SIMILARITY.
 Db 226 SAKSRLQTAPVPMPLKAVNSKGSTENLKHOPGGKVQIINKLDSNVQSKGSNDN 285 PHOSPHORYLATION (BY MARK) (POTENTIAL).
 QY 297 IKHYPGGSVQIVKPVDSLKVSKCGSIGNTIHKPGGQVEVKSEKIDFKDVRQSKIGS 356 PHOSPHORYLATION (BY MARK) (POTENTIAL).
 Db 286 IKHYPGGSVQIVKPVDSLKVSKCGSIGNTIHKPGGQVEVKSEKIDFKDVRQSKIGS 345 PHOSPHORYLATION (BY MARK) (POTENTIAL).
 QY 357 LDNITHVPGGNKIEIHLTLEFRENAKTDHGAEIVKSPVPSGDSPRHISNVNSTGS 416 MISSING (IN TAU-A).
 Db 346 LDNITHVPGGNKIEIHLTLEFRENAKTDHGAEIVKSPVPSGDSPRHISNVNSTGS 405 MISSING (IN TAU-A).
 QY 417 IDMVDSPOLATLADEVASASLAKOGL 441 FC1E79AB CRC32;
 Db 406 IDMVDSPOLATLADEVASASLAKOGL 430
 RESULT 2
 002828 PRELIMINARY; PRT: 402 AA.
 AC 002828: 01-JUL-1997 (Tremblel. 04, Created)
 DT 01-MAY-1999 (Tremblel. 10, Last sequence update)
 DE MICROTUBE ASSOCIATED PROTEIN TAU.
 OS Capra hircus (Goat).
 OC Eutheria; Chordata; Craniata; Vertebrata; Mammalia;
 Caprinae; Capra.
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=RAIN CORTEX;
 MEDLINE: 9701231.
 RA NEILSON P.T.; STEFANSSON K.; GULCHER J.; SAPER C.B.;
 RT Molecular evolution of tau protein: Implications for Alzheimer's
 disease.;
 RL J. Neurochem. 67:1622-1632(1996).
 CC -1- FUNCTION: HEAT STABLE PROTEIN WHICH PROMOTES MICROTUBE ASSEMBLY
 AND STABILITY, AND MIGHT BE INVOLVED IN THE ESTABLISHMENT AND
 MAINTENANCE OF NEURONAL POLARITY. BINDS AND STABILIZES AXONAL
 MICROTUBULES WHICH IS IMPORTANT FOR MAINTAINING AXONAL TRANSPORT
 AND DEFINING THE POLARITY OF A NEURON. AXONAL POLARITY IS
 PREDETERMINED BY TAU LOCALIZATION (IN THE NEURONAL CELL) IN THE
 DOMAIN OF THE CELL BODY DEFINED BY THE CENTROSOME.
 -- SUBCELLULAR LOCATION: MOSTLY FOUND IN THE AXONS OF NEURONS.
 -- ALTERNATIVE PRODUCTS: AT LEAST TWO DIFFERENT ISOFORMS: TAU-A AND
 TAU-B (SHOWN HERE); OF TAU ARE PRODUCED BY DEVELOPMENTALLY AND
 TISSUE-SPECIFICALLY CONTROLLED ALTERNATIVE SPlicing. THEY DIFFER
 FROM EACH OTHER BY THE PRESENCE OR ABSENCE OF TWO EXONS/INSERTS,
 ONE CONTAINING THE ADDITIONAL TAU/MAP REPEAT. SHORT FORMS ALLOW
 PLASTICITY OF THE CYTOSKELETON WHILE LONGER FORMS MAY
 PREFERENTIALLY PLAY A ROLE IN ITS STABILIZATION.
 -- DOMAIN: THE REPEATED DOMAIN Binds TO TUBULIN. TYPE I TAU CONTAINS
 THREE REPEATS WHILE TYPE II TAU CONTAINS FOUR REPEATS.
 -1- PTM: PHOSPHORYLATION AT VARIOUS SERINE AND THREONINE RESIDUES IN
 S-P OR T-P MOTIFS BY RHOINE-DIRECTED PROTEIN KINASES (CDC2, GSK3)
 (A FEW SITES PER PROTEIN IN INTERPHASE, MORE IN MITOSIS), AND AT
 SERINE RESIDUES IN K-X-G-S MOTIFS BY MAP/MICROTUBE AFFINITY-
 REGULATING KINASE (MARK).
 CC -1- SIMILARITY: CONTAINS 4 OR 5 TAU/MAP REPEATS, FROM WHICH ONE IS
 APPROXIMATE, DEPENDING ON THE ISOFORM.
 DR BY SIMILARITY.
 EMBL: S3347; AAB0785; 1.
 PROSITE: PS00229; TAU-MAP; 4.
 DR PFAM: PF00418; tubulin-binding; 4.
 KW Microtubules; Repeat; Alternative splicing; Cytoskeleton; Acetylation;
 Phosphorylation; Init-Motif; Mod-Res; Repet; FT
 FT REPEAT 213 243 TAU/MAP MOTIF.
 FT REPEAT 244 274 TAU/MAP MOTIF.
 FT REPEAT 275 305 TAU/MAP MOTIF.
 FT REPEAT 306 337 TAU/MAP MOTIF.

Query Match 81.8%; Score 1878; DB 6; length 402;
 Best Local Similarity 84.4%; Pred. No. 1. 2e-11; Indels 44; Gaps 4;
 Matches 374; Conservative 8; Mismatches 17; Index 4;
 FT DISULFID 252 283 BY SIMILARITY.
 FT MOD-RES 223 223 PHOSPHORYLATION (BY MARK) (POTENTIAL).
 FT MOD-RES 254 254 PROSPHORYLATION (BY MARK) (POTENTIAL).
 FT MOD-RES 285 285 PROSPHORYLATION (BY MARK) (POTENTIAL).
 FT MOD-RES 317 317 PROSPHORYLATION (BY MARK) (POTENTIAL).
 FT VARSLIC 33 61 MISSING (IN TAU-A).
 FT VARSLIC 236 266 MISSING (IN TAU-A).
 SQ SEQUENCE 402 AA; 41716 MW; FC1E79AB CRC32;

QY 61 SETSDAKSTPTEDVATPLVIDEGAPGKROAQPHTEPEGTAERAGIGTPSLEDAANG 120
 |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
 Db 49 SETSDAKSTPTAE-----AEEAGIGITNSLDQAG 79
 QY 121 HTQARMVSKSDGTGDDDKRAKGACK-TKIAUTPRGAAPPQGQCANTRIPAKTPA 178
 |||||:|||||:|||||:|||||:|||||:|||||:|||||:
 Db 80 HYTOQARMVSKGDGTGDDDKRAKGACK-TKIAUTPRGAAPPQGQCANTRIPAKTPA 178
 QY 179 PRTPPSSGEPPSGDRGSSGSPGPGSTSRSLPTPLTPREPKVAVRTPPKSPSS 238
 |||||:|||||:|||||:|||||:|||||:|||||:
 Db 140 PRTPPSSGEPPSGDRGSSGSPGPGSTSRSLPTPLTPREPKVAVRTPPKSPSS 199
 QY 239 AKSRLQATAPGPMPLKAVNSKGSTENLKHOPGGKVQIINKLDSNVQSKGSNDN 296
 |||||:|||||:|||||:|||||:|||||:
 Db 200 AKSRLQATAPGPMPLKAVNSKGSTENLKHOPGGKVQIINKLDSNVQSKGSNDN 259
 QY 299 HTPGGGVQIVKPVDSLKVSKCGSIGNTIHKPGGQVEVKSEKIDFKDVRQSKIGS 356
 |||||:|||||:|||||:|||||:|||||:
 Db 260 HTPGGGVQIVKPVDSLKVSKCGSIGNTIHKPGGQVEVKSEKIDFKDVRQSKIGS 319
 QY 359 NITHVPGGNKIEIHLTLEFRENAKTDHGAEIVKSPVPSGDSPRHISNVNSTGS 418
 |||||:|||||:|||||:|||||:
 Db 320 NITHVPGGNKIEIHLTLEFRENAKTDHGAEIVKSPVPSGDSPRHISNVNSTGS 379
 QY 419 IDMVDSPOLATLADEVASASLAKOGL 441
 |||||:|||||:|||||:
 Db 380 IDMVDSPOLATLADEVASASLAKOGL 402

RESULT 3
 Q33567 PRELIMINARY; PRT: 686 AA.
 ID 033567: 01-Nov-1996 (Tremblel. 01, Created)
 AC 033567: 01-Nov-1996 (Tremblel. 01, Last sequence update)
 DT 01-Nov-1996 (Tremblel. 12, Last annotation update)
 DE BIG TAU.
 GN TAU.
 OS Rattus norvegicus (Rat).
 OC Eutheria; Rodentia; Sciurognathil; Muridae; Murinae; Rattus.
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE: 92179305.
 RA GOBERT M.; SPILLANTINI M.G.; CROWDER R.A.;
 RT "Cloning of a big tau microtubule-associated protein characteristic of
 the peripheral nervous system";
 RT Proc. Natl. Acad. Sci. U.S.A. 89:1983-1987(1992).
 DR EMBL; M84156; ARB42204; 1.
 DR PROSITE: PS00229; TAU-MAP; 4.
 DR PFAM: PF00418; tubulin-binding; 4.
 KW Microtubules; Repeat; FT
 SEQUENCE 686 AA; 71774 MW; 70992021 CRC32;

Db 34 -----ARVA--SKUKE--DEKKAGDGKTKGAKATPRGAASPAQGTSNATRIPAKT 85
 QY 177 PAPKTPPSSGERPKRSQGDISGYSSPGSGCTPGSJSZPPLPTPPTREPKVAVTRTPRSP 236
 Db 86 PSKTPPPSSGERPKRSQGDISGYSSPGSGCTPGSRSRITSLPDKLNRK 145
 QY 237 SSAKSRLQATPVMPDLKVKSKIGSTENLKHQPGGRQVINKKLDLSNVOSKCGSKDN 296
 Db 146 SASKSRLQATPVMPDLKVRSKIGSTENLKHQPGGRQVINKKLDLSNVOSKCGSKDN 205
 QY 297 IKHVGPGGSVQIVYKPVDLKVTKCGSIGNIHKPGGGQEVKESEKLFKURVOSKIGS 356
 Db 206 IKHVGPGGSVQIVYKPVDLKVTKCGSIGNIHKPGGGQEVKESEKLFKURVOSKIGS 265
 QY 357 LDNITHVPGGGNKRKETKLTERENAKAKTDTGAEIVKSPVPSGDSPRHLNSVSTGS 416
 Db 266 LDNITHVPGGGNKRKETKLTERENAKAKTDTGAEIVKSPVPSGDSPRHLNSVSTGS 325
 QY 417 IDMVDSPOLATLADEVSASLAKOGL 441
 Db 326 IDMVDSPOLATLADEVSASLAKOGL 350

RESULT 8
 02185 PRELIMINARY; PRT; 369 AA.
 ID 02185; PRELIMINARY; PRT; 369 AA.

QY 01-NOV-1996 (TREMBLel. 01, Created)
 DT 01-NOV-1996 (TREMBLel. 01, Last sequence update)
 DE TAU PROTEIN.
 GN TAU.
 OS Bos taurus (Bovine).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
 OC Bovidae; Bos.
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE: 89261765.
 RA HIMMLER A., DRECHSEL D., KIRSCHNER M.W., MARTIN D.W.;
 RT "Tau consists of a set of proteins with repeated C-terminal
 microtubule-binding domains and variable N-terminal domains.";
 RL Mol. Cell. Biol. 9:1381-1388(1989).
 RN [2]
 RP SEQUENCE FROM N.A.
 RX MEDLINE: 89261766.
 RA HIMMLER A.;
 RT "Structure of the bovine tau gene: alternatively spliced transcripts
 of the protein family";
 RL Mol. Cell. Biol. 9:1389-1396(1989).
 DR EMBL; M26178; AA51602.1; -
 DR EMBL; L34940; AA51602.1; JOINED;
 DR EMBL; L34941; AA51602.1; JOINED;
 DR EMBL; L34943; AA51602.1; JOINED;
 DR EMBL; M26178; AA51602.1; JOINED;
 DR EMBL; L34944; AA51602.1; JOINED;
 DR EMBL; L34945; AA51602.1; JOINED;
 DR EMBL; L34946; AA51602.1; JOINED;
 DR EMBL; L34948; AA51602.1; JOINED;
 DR EMBL; L34949; AA51602.1; JOINED;
 DR EMBL; L34950; AA51602.1; JOINED;
 DR EMBL; L34951; AA51602.1; JOINED;
 DR PROSITE; PS00229; TAU-MAP; 4.
 DR PFAM; PF00418; tubulin-binding; 4.
 KW Microtubules; Repeat; 369 AA; 38212 MW; 948F16D CRC32;

QY 02185 PRELIMINARY; PRT; 369 AA.
 ID 02185; PRELIMINARY; PRT; 369 AA.

QY 02188 PRELIMINARY; PRT; 347 AA.
 ID 02188; PRELIMINARY; PRT; 347 AA.

QY 01-NOV-1996 (TREMBLel. 01, Created)
 DT 01-NOV-1996 (TREMBLel. 01, Last sequence update)
 DT 01-NOV-1999 (TREMBLel. 12, Last annotation update)
 DE TAU PROTEIN.
 GN TAU.
 OS Bos taurus (Bovine).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
 OC Bovidae; Bos.
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE: 89261765.
 RA HIMMLER A., DRECHSEL D., KIRSCHNER M.W., MARTIN D.W.;
 RT "Tau consists of a set of proteins with repeated C-terminal
 microtubule-binding domains and variable N-terminal domains.";
 RL Mol. Cell. Biol. 9:1381-1388(1989).
 RN [2]
 RP SEQUENCE FROM N.A.
 RX MEDLINE: 89261766.
 RA HIMMLER A.;
 RT "Structure of the bovine tau gene: alternatively spliced transcripts
 of the protein family";
 RL Mol. Cell. Biol. 9:1389-1396(1989).
 DR EMBL; M26178; AA51605.1; -
 DR EMBL; L34940; AA51605.1; JOINED;
 DR EMBL; L34941; AA51605.1; JOINED;
 DR EMBL; L34944; AA51605.1; JOINED;
 DR EMBL; L34945; AA51605.1; JOINED;
 DR EMBL; L34946; AA51605.1; JOINED;
 DR EMBL; L34948; AA51605.1; JOINED;
 DR EMBL; L34949; AA51605.1; JOINED;
 DR EMBL; L34950; AA51605.1; JOINED;
 DR PROSITE; PS00229; TAU-MAP; 4.
 DR PFAM; PF00418; tubulin-binding; 4.
 DR PROSITE; PS00229; TAU-MAP; 4.
 DR PFAM; PF00418; tubulin-binding; 4.
 KW Microtubules; Repeat; 347 AA; 36016 MW; 00FD6406 CRC32;

Query Match 66.4%; Score 1524; DB 6; Length 369;
 Best Local Similarity 81.8%; Pred. No. 2.5e-89;
 Matches 305; Conservative 6; Mismatches 16; Indels 46; Gaps 5;

QY 1 MAEPRQEEFVMDHAGQDTYGLGDRKGQGYMH-QEGDTAGLKSPLQPTEDSEEP 59
 1 MAEPRQEEFVMDHAGQDTYGLGDRKGQGYMH-QEGDTAGLKSPLQPTEDSEEP 48

QY 60 GSETSDAKSTPPTAEDVTAPEVDEGAPGKQAAQPHETPIEGTAAERAGIDPSLEDEA 119
 Db 49 GETSDAKSTPPE-----AERAGIQTNSLQDQA 79
 QY 120 GIVTOQARNSVKSKRDGSDDKRAGDGK--TKITPRAAAPPGQGOANATRIPAKTP 177
 Db 80 GATIQARNSVKSKRDGIGPDPDKRKTDGADGKPGKTIATPRGAAPPGQGOANATRIPAKTP 139
 QY 178 ARKTPPSSGERPKRSQGRSGSSPGSGTPGSSRSRPSLPTPPTREPKVAVTRTPPKSPS 237
 Db 140 TKTSP--GESGKSGDRGSGYSSPGSGTPGSSRSRPSLPTPPTREPKVAVTRTPPKSPS 97
 QY 238 SAKSRLQATPVMPDLKVTKCGSIGNIHKPGGGQEVKESEKLFKURVOSKIGS 297
 Db 198 AAKSRLQATPVMPDLKVTKCGSIGNIHKPGGGQEVKESEKLFKURVOSKIGS 257
 QY 298 KIVPGGGSVQIVYKPVDLKVTKCGSIGNIHKPGGGQEVKESEKLFKURVOSKIGS 357
 Db 258 KIVPGGGSVQIVYKPVDLKVTKCGSIGNIHKPGGGQEVKESEKLFKURVOSKIGS 317
 QY 358 DNITHVPGGGNKK 370
 Db 318 DNITHVPGGGNKK 330

	Matches	Conservative	Mismatches	Indels	Gaps
Db	1	MAEPROEFDVYMEDHA-----	: : : : :	: : : : :	5;
Qy	60	GSETDAKSTPTAEDVTAPLVDEGAPGKQAAQPHTEIPGTTAEEAGIGDTPLDEAA	: : : : :	: : : : :	59
Db	49	GSETDAKSTPTAE-----	: : : : :	: : : : :	48
Qy	120	GHVTOARMVSKSDGTGSDDKAKAGADK--TKIATPRGAAPPGOKGQANATRIAKTP	: : : : :	: : : : :	59
Db	63	-----ARMVKGDGTGDPDKKTKGADKGKGTKITPRGAAPPGOKGQANATRIAKTP	: : : : :	: : : : :	48
Qy	178	APKTPSSGSPKSKDSDRGSSPGSPGTPOSRSRIPSLPPIPTRPKVAVRTPPKSPS	: : : : :	: : : : :	59
Db	118	TPKTSP--GESSKGDRSGISSPGSPGSRSSRIPSLPPIPTRPKVAVRTPPKSPS	: : : : :	: : : : :	59
Qy	238	SAKSRLQATAVMPDLKVNISKIGTENLKHOPGGKVOLINKKLDLSNVOSKCGSKDN	: : : : :	: : : : :	59
Db	176	AAKSRLQAAAPGMPDLKVNISKIGTENLKHOPGGKVOLINKKLDLSNVOSKCGSKDN	: : : : :	: : : : :	59
Qy	298	KHVPGGGSVQIVYKPVDSLKVTSKGSGLGNIHKGQQEVKSEKLDKFDRVOSKIGL	: : : : :	: : : : :	59
Db	236	KHVPGGGSVQIVYKPVDSLKVTSKGSGLGNIHKGQQEVKSEKLDKFDRVOSKIGL	: : : : :	: : : : :	59
Qy	358	DNTITHVPGGENK 370	: : : : :	: : : : :	59
Db	296	DNTITHVPGGNK 308	: : : : :	: : : : :	59
RESULT	10				
Q28186	ID	PRELIMINARY; PRT; 365 AA.			
AC	Q28186;				
DT	01-NOV-1996 (TREMBLrel. 01, Last sequence update)				
DT	01-NOV-1999 (TREMBLrel. 12, Last annotation update)				
DE	TAU PROTEIN.				
OS	Bos taurus (Bovine).				
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Bovidae; Bovinae; Bos.				
RN	[1]	SEQUENCE FROM N.A.			
RX	MEDLINE; 89261765.				
RA	HIMMELR A., DRICSEL D., KIRSCHNER M.W., MARTIN D.W.;				
RT	"Tau consists of a set of proteins with repeated C-terminal microtubule-binding domains and variable N-terminal domains. ";				
RL	MOL. CELL. BIOL. 9:1381-1388(1989).				
RP	SEQUENCE FROM N.A.				
RX	MEDLINE; 89261765.				
RA	HIMMELR A.; DRICSEL D., KIRSCHNER M.W., MARTIN D.W.;				
RT	"Tau consists of a set of proteins with repeated C-terminal microtubule-binding domains and variable N-terminal domains. ";				
RL	MOL. CELL. BIOL. 9:1381-1388(1989).				
RT	SEQUENCE FROM N.A.				
RT	STRUCTURE OF THE BOVINE TAU GENE: ALTERNATIVELY SPLICED TRANSCRIPTS				
RL	MOL. CELL. BIOL. 9:1389-1396(1989).				
DR	EMBL; M26178; AAA51604.1; JOINED.				
DR	EMBL; L33940; AAA51604.1; JOINED.				
DR	EMBL; L33941; AAA51604.1; JOINED.				
DR	EMBL; L33944; AAA51604.1; JOINED.				
DR	EMBL; L33946; AAA51604.1; JOINED.				
DR	EMBL; L33947; AAA51604.1; JOINED.				
DR	EMBL; L33948; AAA51604.1; JOINED.				
DR	EMBL; L33949; AAA51604.1; JOINED.				
DR	EMBL; L33950; AAA51604.1; JOINED.				
DR	EMBL; L33951; AAA51604.1; JOINED.				
DR	PROSITE; PS00229; TAU_MAP; 4.				
DR	PFAM; PF00418; tubulin-binding; 4.				
KW	Microtubules. Repeat; SEQUENCE; 365 AA; 37923 MW; 08A4187E CRC32;				
SQ	SEQUENCE 338 AA; 34965 MW; F349F977 CRC32;				

Query Match Score 1410; DB 6; Length 365;
Best Local Similarity 73.5%; Pred. No. 4e-82;

Fri Sep 29 08:18:21 2000

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